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May 20, 2003, 16:59:45 ; Search time 75 Seconds (without alignments) 365.995 Million cell updates/sec
                                                                                                                                                                                                      US-09-887-855-5
1115
1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                Perfect score:
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                                                                                                                                                                                                                                                  Sequence:
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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

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SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*

SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*

SIDS2/gcgdata/geneseqy-embl/AA1990.DAT:\*

SIDS2/gcgdata/geneseqy-embl/AA1990.DAT:\*

SIDS2/gcgdata/geneseqy-embl/AA1990.DAT:\*

SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Amino acid sequenc Human extracellula Human novel polype Human polypeptide Human protein sequ Human secreted pro Amino acid sequenc Human PRO 234 prote Human PRO234 prote
SUMMARIES	AAY93948 AAE03651 ABG66680 AAB90203 AAA2796 AAY1490 AAY1367 AAU29033 AAB80235
0.03	22 22 22 22 22 23
% Query Match Length DB	374 374 374 374 382 382 382 382 382 382
% Ouery Match	100.0 100.0 100.0 100.0 99.1 98.7 98.7 98.7
Score	1115 1115 1115 1115 1115 1105 1101 1101
Result No.	10 6 4 7 9 6 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

98US-0113820.

22-DEC-1999; 23-DEC-1998;

06-JUL-2000.

(IMMV ) IMMUNEX CORP.

Human PRO1890 poly	PRO1890.	7				Peptide #3978 enco	~	Human secreted pro		Soluble mannose re	Novel human diagno	Murine macrophage	Human novel extrac	Human polypeptide	type	Human ORFX ORF2915	Human type C lecti	Human Tumour Endot	Human novel extrac	Human polypeptide	Novel human diagno	Human versican iso	Human cancer assoc	Neurocan core prot	Versican. Homo sa	Murine type C lect	Murine E-selectin	Mouse Tumour Endot	Amino acid sequenc	Mouse protein enco	Human DC-SIGN prot	Mouse cell surface	Haematopoietic ste	
AAU12441 AAB73309	AAB8760	ABB9555	ABB8494	AAB941	ABB2178	AAM2994	AAY9164	AAY9155		AAR2403	ABG2072	AAB23824	AAU1963	ABP4785	AAW4411	AAB4315	AAB2382	ABB9075	AAU1978	ABP4800	ABG2072		•	<b>AAR4662</b>	AAR1260		AAB2382	ABB9078	AAG6334	AAU880	AAU8802	¥	AAY7918	
22	22	23	23	22	22	22	21	21	21	13	22	21	22	23	18	21	21	23	22	23	22	23	21	15	12	18	21	23	22	23	23	21	21	
273	273	273	273	232	102	102	81	82	115	1456	1184	1455	250	250	1479	1479	1479	1479	154	154	290	655	741	1257	2409	1479	1479	1479	742	325	325	637	644	
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561.5	61.	61.	61.	94	275	275	240	240	240	183	18	78.	76.	76.	76.	ė.	76.	76.	75.	75.	175	174	174	174	17	170.5	9.	70.	65.	158	15	153.5	53.	
11	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

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/note= "signal peptide"
22..27
/note= "extracellular coding region"
228..28
/note= "predicted transmembrane domain"
249..374
/note= "predicted cytoplasmic or intracellular domain"
                                                                 Amino acid sequence of a lectin ss3939 polypeptide.
                                                                                  Human; lectin ss3939; chromosome 11; gene therapy.
                                                                                                                  Location/Qualifiers
               AAY93948 standard; Protein; 374 AA.
                                                 (first entry)
                                                                                                                                                                                                   WO200039296-A1.
                                                                                                   Homo sapiens,
                                                 03-OCT-2000
                                AAY93948;
                                                                                                                  Key
Peptide
                                                                                                                                          Domain
                                                                                                                                                            Domain
                                                                                                                                                                           Domain
RESULT 1
       AAY93948
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Protein
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                                                                                                                                                                                                                                                                                      present sequence represents a human lectin ss3939 polypeptide. The
                                                                                                                                                                                                                                                                                                             polynucleotide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map geneme on human chromosome number 11, to sense or antisense associated with chromosome 11, as single-stranded sense or antisense oligonucleotides to inhibit expression of polypeptides encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides may be useful for developing treatments for diseases (none specified) associated with defective or insufficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGRILSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human extracellular matrix and cell adhesion molecule-15 (XMAD-15)
                                                                                                                                                  ss3939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1115; DB 21; Length 374; 100.0%; Pred. No. 3.5e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amounts of the polypeptides. The antibodies may be useful for detecting the presence of ss3939 polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 LPEETQEEDAKKTFKESREAALNLAY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE03651 standard; Protein; 374 AA.
                                                                                                                                                                                                                                  Claim 12; Page 8; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                  2000-452394/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA;
                                                                                           N-PSDB; AAA57382
                 Anderson DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3est Local Sim
4atches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE03651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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ID AAE03651
XX AC AAEC
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XX XX HUMM
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AGTOIN

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Location/Qualifiers 1..24

Peptide

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diffectiveness as an agonist or antagonist of XMAD. The identified agonist of adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally correct a genetic deficiency, to express a conditionally consistent intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating comparisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human diseases. Oligonucleotide or longer fragments derived from the polynucleotide sequences may be used as elements on a microarray. Antibodies which specifically bind XMAD may be compared for the diagnosis of disorders associated with the expression of XMAD, or in assays to monitor patients being treated with XMAD. Diseases of advanced any procession of transfer and procession of the diagnosis of disorders associated with the expression of advanced procession of transfer and procession of the diagnosis of disorders deferted effects the diagnosis of disorders associated with the expression of advanced procession of the diagnosis of disorders deferted effects of the diagnosis of disorders deferted effects associated with the analysis of disorders associated with the expression of advanced procession of the diagnosis of disorders associated with AMAD. Diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle cell anemia, thalassaemia, autoimmune/inflammatory disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, allergies, anaemia, asthma atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders.
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                                                                                                            "Mature human extracellular matrix and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 P, Burford N, Azimzai Y, Patterson C;
Shah P, Au-Young J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is a human extracellular matrix and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                     "C-type lectin domain"
                                                                                                                                                                                                                                                                                                                   "C-type lectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                      /note- "Transmembrane motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Transmembrane motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                            adhesion molecule (XMAD)"
/label- Signal_peptide
25..374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 108-109; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0172852.
99US-0172354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             . . 348
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Best Local Similarity 100.
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                   ..247
                                                                              25..374
/note-
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                                                                                                                                                                                                   46..63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H, Tang YT, La
Baughn MR, Lu DAM,
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                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, tissue repair, healing of burns, incisions, ulcers, treatment of osteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia garvis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG66758 represent human novel polypeptides of the invention.

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Gaps

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Indels

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Conservative

Best Local Similarity Matches 206; Conserv

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374 AA;

Sequence Query Match

100.0%; Score 1115; DB 23; Length 374; 100.0%; Pred. No. 3.5e-105;

61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120

1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60  82 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 141

121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180 

202 181

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ABB90203 standard; Protein; 374

ABB90203

ABB90203;

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cancer; wound healing; central nervous system disease; haematopolesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; plantelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; allorgic condition; thrombolysis; thrombolysis; coagulation disorder; fungal infection.
                                                                                                                   IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
                                                                                                                                                                                                                                       CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                                                                                                                                                                                                                                                      142 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 201
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                            22 ATGRILISGOPVCRGGTORPCYKVIXFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                  ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition; shock; sepsis; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asundi V, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۵,
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Drmanac 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG66680 standard; Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel polypeptide #15.
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Yamazaki V, Ujwal ML,
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ANG 66680

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                         Human polypeptide SEQ ID NO 2579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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   (first entry)
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N-PSDB; ABL90612.
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24-MAY-2002
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Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -

N-PSDB; ABK94904

Claim 10; Page 579-580; 672pp; English.

The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischemania-reperfusion influry, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and brain tissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemotactic or chemokinetic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia,

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB8040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are solutions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's classe, multiple asclerosis, rheumatoid arthritis and ulcerative (d) wound healing; (e) infectious diseases such as myocardial ischaemia; epilepsy; and (f) infectious diseases such as myocardial fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; Parkinson's disease; neurodegenerative disorder;
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Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and parasitic infections.
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AAM25965. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinfinamatory; antinfheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; antianamanic; antianamanic; antianamanic; antianamanic; antianamanic; antianamanic; antialorer; categoraphic; dermatological; antialorgic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; contidiates or antidiapostimulant; The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antidonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders, canemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema allergic fibritis, asthma, diabetes, cancer, multiple sclerosis, depression, allowed the antidepression, allowed the antidepression, neuroperpenders, cancer, multiple sclerosis, depression, allowed the antidepression neuroperpenders and antidepression, allowed the antidepression, allowed the antidepression neuroperpenders.
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                                                                                                                                                                                                                                                                                                                                                                Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1115; DB 22; Length 387; 100.0%; Pred. No. 3.6e-105; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 272; 1217pp; English.
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                                                                 22-DEC-2000; 2000WO-US35017.
                                                                                                          23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                     26-JUL-2001.
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22 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 81

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Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
antiHIV; antiInflammatory; nootropic; neuroprotective; antiallergic;
osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
immune disease; inflammation; blood disorder; tumour.
                                                                                                                                                                                                                                                                                                                                            encode,
        Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encouseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                   Moore PA,
E, Brewer
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98US-0095486.
98US-0095454.
98US-0095455.
98US-0096319.
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                                                                                            Homo sapiens.
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12-AUG-1998
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The polynuclectide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted complete in Examples of the activities are: cytostatic; they are antiallarished; contablergic; osteopathic; antiarthritic; antibacterial; antidabetic; antiasthma; antipsoriatic; and cardiant. The polynuclectides and their corresponding secreted proteins are useful for preventing, treating or ameliorating madical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynuclectides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, developmental abnormalities and foetal deficiencies, and behavioural disorders, schizophrenia, costeoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, psoriasis, cardiovascular disorders and metabolic disorders. The proteins cord injuries, cordinar septiatory disorders and metabolic disorders. The proteins cordinaries, cordinaries, are also be useful for identifying their binding partners.
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ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60 Length 374; 2; Indels Score 1105; DB 21; Pred. No. 3.6e-104; 0; Mismatches 99.18; 99.08; tches 204; Conservative Similarity Query Match Local -

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CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPV 180
                                              Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psorlasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
          IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV
                                                                                                                                                                                                                Secreted protein; transmembrane protein; human; enterocolitis;
                                                                                                                                                                                             Amino acid sequence of protein PRO234
                                                                         LPEETQEEDAKKTFKESREAALNLAY 206
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                                                                                  AAY13367 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                      970S-0059113.
970S-0059115.
970S-0059117.
970S-0059119.
970S-0059121.
970S-0059128.
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9708-0059266.
9708-0062125.
9708-0062287.
9708-0062814.
9708-0062814.
9708-0062816.
9708-0063106.
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970S-0063128.
970S-0063329.
970S-0063327.
970S-0063541.
970S-0063542.
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97US-0063732
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                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                         WO9914328-A2
                                                                                                                                                                                                                                                                                                                                             16-SEP-1998;
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24-OCT-1997;
24-OCT-1997;
27-OCT-1997;
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29-0CT-1997;
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28-OCT-1
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202 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 235
                                                                                                                                AAU29033 standard; Protein;
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30-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan J,
                                                                                   RESULT 8
            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY13344-403 represent secreted and transmembrane human proteins.
The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal lung, fetal town of fetal facina.
The encoded polypeptides have specific uses based on their homology to represent the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosa lesions associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosa lesions (e.g. enterocolitis, zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skind diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, als, neuropathies or cancer. PRO255 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO256 can be used as a a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO353 can be used as an anti-thrombotic agent; PRO387 polypeptides and portions may have therapeutic applications in wound healing and tissue repair: PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood versels, or related tissue, e.g. in the heart of genital tract.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 141
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                                                                                             970S-0063870.
970S-0064103.
970S-006428.
970S-0065809.
970S-0065186.
970S-0065846.
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97US-0066364.
                              97US-0063734
97US-0064215
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97US-0066770
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97US-0066453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-229533/19.
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Matches 206; Conserv
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29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
12-NOV-1997;
11-NOV-1997;
11-NOV-1997;
21-NOV-1997;
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dog, cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney AL;
                                                         PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski PJ,
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امما WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI,
                                      Human PRO polypeptide sequence #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen J, Desnoyers L,
ith V, Watanabe CK, W
                                                                                                                                                                                                                                                   2000US-1908289
2000US-1910AP
2000US-1910AP
2000US-19265P
2000US-19363P
2000US-19363P
2000US-19444P
2000US-19464P
2000US-194647P
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2000US-196187P.
2000US-196690P.
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2000US-198121P.
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2000US-199397P.
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2000US-199654P.
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2000WO-US34956
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                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS45934
                                                                                                                          WO200168848-A2.
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28-WAR-2000;
28-WAR-2000;
29-WAR-2000;
30-WAR-2000;
30-WAR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
11-APR-2000;
25-APR-2000;
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Sequences AAU29024-AAU29128 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumnour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal expression in the test sample indicates the presence of a tumnour in the expression in the test sample indicates the presence of a tumnour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumnour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumnours and also proteins can be used to determine the presence of tumnours and also breast, prostate, rectal, cervical, or liver tumnours, in mammalian content subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
             Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory; antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 382;
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Pred. No. 9.5e-104;
0; Mismatches 0;
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                                                                                     Claim 11; Fig 20; 774pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.7%;
Best Local Similarity 96.3%;
Matches 206; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                        382 AA;
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple solerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum.
                                                                                                                                                                                                                                                                                                                                                       Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ; Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use as hybridization probes, and in chromosome and gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1101; DB 22;
Pred. No. 9.5e-104;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 50; 393pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18913 standard; Protein; 273
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                                                                                99WO-US23089.
                                                                                                                                          99WO-US30911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.7%;
ilarity 96.3%;
Conservative
                                         99WO-US20944.
                                                                                                              99WO-US28313,
                                                                                                                           99WO-US30095
                           99WO-US20594
                                                                                                                                                      99WO-US30999
99WO-US00219
                                                                     99WO-US21547
                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                   Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease)
                                                                                                                                                                                                                                                                                                             2001-081051/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF72396.
                                                                                                                                                                                                                                                                                 Williams PM,
                                      13-SEP-1999
15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
29-NOV-1999;
                                                                                                           30-NOV-1999;
16-DEC-1999;
20-DEC-1999;
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Best Local Simi
Matches 206;
                          08-SEP-1999;
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ID AAB1
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AC AAB1
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                                                                                                                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; PR01484; PR04334; PR01122; PR01889; PR01889; PR01887; PR041785; PR04353; PR04405; PR04405; PR04356; PR04352; PR04354; PR04425; PR04425; PR04425; PR04422; PR04424; PR04424; PR04422; PR044430; PR04499; tunnour; obesity; diabetes; Insullnemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; cellac disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan
                                                                                                                                                                                                                                                                                         "CAMP- and cGMP-dependent protein kinase phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski PJ,
                                                                                                                                        'note- "N-myristoylation site"
                                                                                                                                                66..71
/note- "N-myristoylation site"
                                                                                                                                                                                   /note- "N-myristoylation site"
                                                                                                                                                                                                 /note= "N-myristoylation site"
                                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                               /note= "N-myristoylation site"
                                                                                                                                                                                                                                             "N-myristoylation site"
                                                                                                                                                                                                                                                                          'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Z;
                                                                                                                                                                     note- "Glu encoded by CAA"
                                                                                                                                                                                                                                                            "N-myristoylation
                     novel polypeptide designated PR01890.
                                                                                                                           /note= "signal peptide"
                                                                                                            Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard A,
Wood WI,
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99US-0125878.
99US-0125826.
99US-0127035.
99US-0131270.
99US-0131272.
99US-0131272.
99US-0131273.
99US-01312371.
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99US-0144791.
99US-0146970.
99US-0170262.
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      08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eaton DL, G
Watanabe CK,
                                                                                                                                                                                                         102..107
/note= "N
                                                                                                                                                                                                                       ..114
                                                                                                                                                                                                                                      .145
                                                                                                                                                                                                                                                    .217
                                                                                                                                                                                                                                                                                 ..269
                                                                                                                                                                                                                                                                  214..235
                                                                                                                                                                             96..
                                                                                                                                                                                           93..98
                                                                                                                                                                                                                                              note-
                                                                                                                                                                                                                                                             'note-
                                                                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                        109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-628263/60.
N-PSDB; AAA96340.
                                                                                                                                                              Misc-difference
                                                                                 Crohns disease
                                                                                                                                                                                                                                                                                                               WO200056889-A2.
                                                                                                                                 Modified-site
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                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                           01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                          23-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999
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03-AUG-1999,
                                                                                                                                                                                                                                                                                                                             28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                        24 - MAR - 1999
                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-1999
                                                                                                                   Peptide
                                                                                                                                                                                                                                                                   Domain
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The present sequence represents a secreted or transmembrane polypeptide.
The specification describes polypeptides designated PR01484, PR04334,
PR01125, PR01889, PR01890, PR0185, PR04557, PR04405,
PR01125, PR04356, PR04380, PR04480, PR05187, PR04457, PR04405,
PR041356, PR04424, PR04422, PR04430 and PR04499, PR051889 polypeptide is
useful for diagnosing tumour in a mammal. The polypeptides, their
agonists and antagonists are useful treating a condition associated with
expression or activity of the polypeptide. Conditions treated include
obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
capable of inducing proliferation of mammalian kidney mesangial cells
and are therefore useful for treating a Bergers disease or other
cheropathies associated with Schonlein-Henoch purpura, celiac disease,
dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
to generate transgenic animals for use in development and screening of
therapeutically useful reagents and also for chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 RVVSGQKVCFADFKHPCXKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.4%; Score 561.5; DB 21; 60.1%; Pred. No. 7e-49; iive 25; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1890 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU12441 standard; Protein; 273 AA
                                                                                                                            Claim 12; Fig 10; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US28634
99WO-US28551.
99WO-US28564.
99WO-US28565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.1%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200140466-A2
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02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
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Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO Polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                          Deforge L, Desnoyers L, Filvaroff E, Ga
V, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                               Tumas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 540; 813pp; English.
                                                           2000WO-US04341
                                                                     2000WO-US04342
                                                                                                                                                2000WO-US14042.
2000WO-US14941.
                                                                                             2000WO-US05004
                                                                                                                        2000WO-US07532
                                                                                                                                 2000WO-US08439
                                                                            2000WO-US04414
2000WO-US04914
                                  2000WO-US00277
                                                                                                                                                                   2000WO-US15264
                                                                                                                                                                            2000WO-US30873
                                                                                                               2000WO-US07377
                                                                                                                                                                                                             Baker KP, Beresini M,
Gerritsen ME, Goddard
                                                                                                                                                                                                                                Stewart TA,
                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                               WPI; 2001-408281/43.
                                                                                                                                                                                                                                                        N-PSDB; AAS21513
                       30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
                                                                  18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
30-MAR-2000;
                                                                                                                                       17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
                                                                                                                                                                                                                                Smith V,
```

Adul2172-Adul2446 represent novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
Dreast, prostate, rectal, cervical or liver tumours by comparing PRO
Dreast, prostate, rectal, cervical or liver tumours by comparing PRO
Collypeptide expression in a cell sample to that in a control sample.
Come of the 275 sequences are also useful to stimulate the release of
Cumour necrosis factor-alpha (TNF-alpha) from human blood, the
Common periorite cells, the release of proteoglycans from
Cartilage, the proliferation of inner ear utricular supporting cells of
Cortilage, the proliferation of inner ear utricular supporting cells or
Cortilage, the proliferation of endothelial cells. Some of
Cortilage, the proliferation of endothelial muscle cells or by adipocytes; or inhibit binding of A-peptide
Cortilage, and the used to generate probes, antisense RNA/DNA,
Cransgenic or knock out animals and can be used in gene therapy.

273 AA; Seguence

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ë
                                           Gaps
     DB 22; Length 273;
50.4%; Score 561.5; DB 22; Length: 60.1%; Pred. No. 7e-49; Live 25; Mismatches 35; Indels
                                  Matches 101; Conservative
 Query Match
Best Local Similarity
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RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63 4

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- 64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118 ò g

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119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
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AAB73309 standard; Protein; 273

AAB73309 ID AAB7

(first entry)

22-MAY-2001

AAB73309;

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New PC-LECTIN polynucleotide encoding a transmembrane antigen over expressed in human prostate cancer, useful for the prognosis, diagnosis and treatment of prostate cancer
                                                      Human; PC-LECTIN; C-type lectin; transmembrane antigen; normal testis; layilin homologue; prostate cancer antigen; overexpression; androgen-dependent prostate cancer; diagnosis; prognosis.
                                       Human C-type lectin transmembrane antigen PC-LECTIN, SEQ ID NO:2.
                                                                                                                                                                                   Afar DEH, Hubert RS, Jakobovits A, Raitano AB;
                                                                                                                                     11-AUG-2000; 2000WO-US22065.
                                                                                                                                                    99US-0148935.
                                                                                                                                                                    (UROG-) UROGENESYS INC.
                                                                                                                                                                                                  WPI; 2001-211222/21.
N-PSDB; AAF76004.
                                                                                                     WO200112811-A1.
                                                                                       Homo sapiens.
                                                                                                                                                    12-AUG-1999;
                                                                                                                      22-FEB-2001.
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3

Claim 1; Fig 1A-D; 116pp; English.

The invention relates to a novel human C-type lectin transmembrane antigen, PC-LECTIN (AAB73309) and cDNA encoding it (AAF76004). The expression of the human PC-LECTIN gene is normally restricted to the testis, but is highly overexpressed in prostate cancer. PC-LECTIN expression is highly overexpressed in prostate tumours compared with androgen-independent prostate tumours, and expression is therefore likely to be dependent on the presence of androgen dependent prostate cancer. PC-LECTIN therefore represents a diagnostic and therapeutic target for prostate cancer, particularly androgen-dependent prostate cancer. Human PC-LECTIN therefore represents to thought to be the human orthologue of 1941lin, as diverges significantly in a key functional domain or proposed for the layilin protein. Human PC-LECTIN or immunogenic portion thereof, a vector encoding PC-LECTIN or immunogenic portion thereof, a vector encoding PC-LECTIN, a PC-LECTIN antisense nucleotide, a PC-LECTIN nucleotide-targetted ribozyme, or an anti-proposed for a PC-LECTIN nucleotide-targetted ribozyme, or an anti-proposed for that order of particularly prostate cancer, but also breast, bladder, lung, bone, colon, pancreatic, testicular, cervical or bladder, lung, bone, colon, pancreatic, testicular, cervical or useful for diagnosis and/or prognosis of prostate cancer. PC-LECTIN antibodies and nucleotides are useful in the treatment (e.g., antisense therapy), engagence of encered and other PC-LECTIN and diagnosis and/or prognosis of prostate cancer and other PC-LECTIN and particular, expressing cancers. PC-LECTIN antibodies may also be used as drug additional to the prostate cancer and other PC-LECTIN and particular, and particular and particul over targetting agents. The PC-LECTIN nucleotides and proteins may additionally be used in drug discovery to identify molecules the modulate PC-LECTIN function or expression. The present sequence

273 AA; Seguence

22; Length 273; DB 50.4%; Score 561.5;

Gaps

1,

Indels

Length 273;

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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary;
                                                                                                                                                                64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                                                                  83 MLQNLTKPGTGISDGDFWIGLWRNGDGQT-SGACPDLYQWSDGSNSQYRNWYTDEPSCGS 141
                                                                                                                      23 RVVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENBAEQKLIES 82
                                                                                                    4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiogenesis related protein PRO1890 SEQ ID NO: 264.
                                                                                                                                                                                                                             119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                            142 EKCVVWYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP 189
                                    DB 22;
                                                                  35;
                                   50.4%; Score 561.5; DB 60.1%; Pred. No. 7e-49; iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                          ABB95554 standard; Protein; 273
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2000US-0664610.
2000US-0665350.
2000US-242922P.
2000US-0709238.
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2000WO-US30873.
2000WO-US32678.
2000US-0747259.
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2001US-0767609.
2001US-0796498.
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2000WO-US20710.
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2000US-230978P
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2001WO-US06666.
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001US-0808689
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2001US-0866034
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                                                   Best Local Similarity' 60.1%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic
        273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200208284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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01-DEC-2000;
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20-DEC-2000;
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28-FEB-2001;
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22-MAR-2001;
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25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                           ABB95554;
        Sequence
                                    Query Match
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                                                                                                                                                                                                                                                                                                             RESULT 14
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                                                                                                          64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                  Gaps
                                                                 23 RVVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES 82
                                                4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
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Wood WI;
                                                                                                                                                                           119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                            142 EKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP 189
                35; Indels
   Pred. No. 7e-49;
                  25; Mismatches
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Watanabe CK,
                                                                                                                                                                                                                                                                                      AAB87609 standard; Protein; 273 AA
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2000WO-US04414.
2000WO-US05601.
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990S-0170262.
20000S-0175481.
60.18;
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25-APR-2000; 2000US-0199397.
22-MAY-2000; 2000WO-US14042.
05-JUN-2000; 2000US-0209832.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO protein; mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2000; 2000WO-US23328
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99WO-US21090
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
 Best Local Similarity 60.1
Matches 101; Conservative
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J, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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11-JAN-2000; 2
18-FEB-2000; 2
18-FEB-2000; 2
22-FEB-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                   Human PRO1890
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Grimaldi CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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15-SEP-1999;
07-DEC-1999;
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AAB87609;

RESULT 13 AAB87609

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Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; mycardial infarction; thrombophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antianglogenic, hypotensive, vulnerary and antiarteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paon1 NF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME,
            Human PRO1890 protein sequence SEQ ID NO:264
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L, Hillan KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US2332B
2000US-239978P
2000US-0664510
2000US-24292P
2000US-070923B
2000WO-US30952
2000WO-US30953
2000WO-US30873
2000WO-US30873
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2000WO-US30873
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2000WO-US30873
2000WO-US30873
2001WO-US30873
2001WO-US06520
2001WO-US06520
2001WO-US06520
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2001US-0854208.
2001US-0854280.
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2000US-222695P.
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2001US-0866034
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JF, Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-090516/12.
N-PSDB; ABL88203.
                                                                                                                                                                                                                                                                                                                   WO200200690-A2.
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20-DEC-2000;
20-DEC-2000;
22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
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09-MAR-2001;
14-MAR-2001;
22-MAR-2001;
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18-SEP-2000;
18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
08-NOV-2000;
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23-AUG-2000;
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10-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski
                                                                                                                                                                                                                                                                       Homo
         NEW YORK WENT WENT WAS A STREET OF THE WAS A S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thombophlebitis, lymphangitis, tumnour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.4%; Score 561.5; DB 23; Length 273; 60.1%; Pred. No. 7e-49; ive 25; Mismatches 35; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rber H, Gerritsen ME, Goddard A;
Hillan KJ, Marsters SA, Pan J,
Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 264; 567pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerber H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB84948 standard; Protein; 273
25-MAY-2001; 2001WO-US17092.
30-MAY-2001; 2001WS-0870574.
30-MAY-2001; 2001WO-US17443.
01-JUN-2001; 2001WO-US17800.
20-JUN-2001; 2001WO-US19692.
28-JUN-2001; 2001WO-US00000.
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Godowski PJ, Gurney .....
TF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                         BAKER K P.
FERRARA N.
GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                              GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                   GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL95692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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(HILL/)
(MARS/)
(PANJ/)
(PAON/)
(STEP/)
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(GODD/)
(GODO/)
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                                                                                                                                                                                           BAKE/)
                                                                                                                                                                                                                                       GERB/)
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activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothellal or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosolerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycocardial infarctions, thrombophlebitis, lymphangitis, tumour anglogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular bilogy, including use as hybridisation probes, and in chromosome and gene mapping. ABL081259 to ABL881267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.4%; Score 561.5; DB 23; Length 273; Best Local Similarity 60.1%; Pred. No. 7e-49; Matches 101; Conservative 25; Mismatches 35; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 20, 2003, 17:05:07 Job time: 77 secs
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May 20, 2003, 17:03:50 ; Search time 15 Seconds (without alignments) 404.075 Million cell updates/sec
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1115
1 ATGRILSGQPVCRGGTQRPC.......EEDAKKTFKESREAALNLAY 206
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/PCTUS\_COMB.pep:\*

# Result Ouery Ouery Duery Duery

Sequence 8, Appli Sequence 11, Appl Sequence 17, Appl Sequence 20, Appli Sequence 2, Appli Sequence 5, Appli Sequence 13, Appli Sequence 9, Appli Sequence 9, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 27, Appli		B 3; Length 1455; 10; 66; Indels 53; Gaps 8; LIERFIENLLPSDGDFWIGLR 80 :             FLWRYI-NKNGGQSPYFIGML 864 -EVCVVWYHQPSAPAGIGGPY 138
4 US-09-535-521-8 4 US-09-535-521-11 4 US-09-535-521-17 4 US-09-535-521-27 4 US-09-535-521-2 4 US-09-535-521-2 5514582-9 5514582-9 1 US-08-310-294-9 1 US-08-310-294-9 4 US-09-11-470-6 1 US-08-310-534-16 1 US-08-310-534-16 1 US-08-310-534-16 1 US-08-310-534-16 1 US-08-310-334-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16 1 US-08-314-394-16	ALIGNMENTS S/08840062 S/08840062 TEENCE A. TYPE C LECTINS 15 i, Inc. an Bruno Blvd ncisco ncisco ch, 1.44 Mb floppy disk mpatible cc. TOOS/MS-DOS (Genentech) TA: TOOS/MS-DOS (Genentech) TA: TOOS/MS-DOS TA: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MATION: TOOS/MS-MS-MS-MS-MS-MS-MS-MS-MS-MS-MS-MS-MS-M	Q ' X — X '
12.1 12.1 13.9 12.1 13.1 12.1 12.1 12.1 12.0 12.0 13.3 12.0 13.3 12.0 13.0 13.0 13.0 13.0 13.0 13.0 13.0 13	ication U TION: ASKY, LAU WINEN: TUENCES: E ADDRESS Genentec Genentec Genentec Genentec Genentec Genentec Genentec Genentec Genentec ABLE FORM: SYSTEM: FYSTEM: NUMBER: IN NUMBER: IN NUMBER: OCKET NUM NUMBER: OCKET NUM ACTERISTI A31-7168 SEQ ID N ACTERISTI SS amino	tch al Similarity 25.9%; Pred. No. 8.3e 53; Conservative 33; Mismatches YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQ    ::
288 339 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 3310 33	RESULT 1 US-08-040-062-5 Sequence 5, Appl Patent No. 61179 GENERAL INFORMATION TITLE OF INVE NUMBER OF SEG CORRESPONDENC ADDRESSEE: STREET: 46 COUNTY: W COUNTY: W COUNTY: W COUNTY: OF SEG SOFTWARE: COMPUTER FRAD MEDIUM TYPE COMPUTER: OPERATING SOFTWARE: COMPUTER: OFFRATING SOFTWARE: COMPUTER: OFFRATION FOR SEGISTRATION FOR SEGISTRATION FOR SEGISTRATION FOR SEGUENCE/P TELEFRAX: 4 TELEFAX: 4 TELEFAX: 910 INFORMATION FOR SEGUENCE CHAR.	Query Match Best Local S1 Matches 53;  Qy 21 YKVIY  Db 806 YKDYQ  QY 81 RREEK

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865 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY----TNSGF---- 907
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                                    139 MFQWNDDRCNMKNNFICK---YSDEKPAVPSREAEGEETELTTPVLPEETQE-----
                                                                         ----TTPTTPGGCKEGWHLYKNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%; Score 176.5; DB 3; 30.4%; Pred. No. 1.4e-09; tive 25; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFFWARE: WinPatin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
                                                             908 ---WNDINCGYPNNFICQRHNSSINATAMP
                                                                                                                                                                                                                                                                                         APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
WUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
SYREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P1019R1
                                                                                                          188 ----- EDAKKTFKESREALNL 204
                                                                                                                                            954 CFKIFGFANEEKKSWQDARQACKGL 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/08340428B Patent No. 5648465
GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 4, Application US/08840062
Patent No. 6117977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-3216
TELEPA: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
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Amino Acid
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Matches 51, Conservative
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 133
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: RAUCH, Uwe
APPLICANT: WARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEPROCAN AS A CHONDROITIN SULFATE PROTEOCLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broady and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 15.6%; Score 174; DB 1; Length 1257; Best Local Similarity 30.8%; Pred. No. 2e-09; Matches 44; Conservative 18; Mismatches 49; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RUOSLAHII, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
ANTIBODIES, AND METHODS OF DETECTING THE SAME
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/441,179
FILING DATE: 27-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 NO. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margolis-1A
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REFERENCE/COCKET UNBER: Max
TELECOMMUNICATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1257 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                             U.S.A.
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5180808-2
; Patent No. 5180808
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                                                                                                       76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 QEVE---ELMIGL------NDLKLQMNFEWSDGSLVSFTHWHPFEPNNFRDSLEDCVT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 SWQPF-----QGHCYRL-----QAEKRSWQESKRACLRGGGDLLSIHSWAELEFITKQIK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                              Gaps
                                                                             17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                            40;
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15.6%; Score 174; DB 6; Length 2409;
28.5%; Pred. No. 4.9e-09;
Live 23; Mismatches 55; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Indels
                                                                                                                                                                                                                                                                    -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2323
                                                                                                                                                                                                                                         132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 170.5; DB 3
Pred. No. 5.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELEPHONE: 415/225-3216
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08840062 Patent No. 6117977
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1479 amino acids
                  Best Local Similarity 28.5
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 31.4
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                             US-08-840-062-2
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  Query Match
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697 QGACYK----HFSARR-SWEEAENKCRMYGAHLASISTPEEQLFINNRYREYQ------# 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.446C5
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Indels
                                                                        APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 GIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEG 171
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
                                                                                                                                                                        ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.6%; Score 152; DB 5; Best Local Similarity 28.8%; Pred. No. 2.6e-07; Matches 47; Conservative 17; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FP-LJ 1453
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         : Sequence 2, Application PC/TUS9503747
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99, Application US/09602877A Patent No. 6432707 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION UNDRER: 37,643
REFERENCE/DOCKET NUMBER: FP-L.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 912 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / MOLECULE TYPE: protein
PCT-US95-03747-2
                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                         CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                            USA
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PCT-US95-03747-2
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Indels

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74 IGLRNLDLKGE-----FIWVDGSHVDYSNWAPGEPTSRSQGEDCVMM-----RGS 118
                                                                                                                                                                                                                                                       77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGI 134
                                                                                                                                                                                                                             135 GGPYMFQWNDDRCNMK-NNFICKYSDEKPAV---PSREAEGE------ETELTTPV 180
                                                               17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                      24 ORKCY---YFGKGTKQ--WVHARYACDDMEGQLVSIHSPEEQDFLTKH----ASHTGSW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Irving M. Fishman, CIBA-GEIGY Corporation
556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Debre, Patrice
APPLICANT: Mossalayi, Mohammed D
TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human B. Cells
CHO cells transformed with pCAL8-BF-ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
    Best Local Similarity 30.2%; Pred. No. 5.7e-08; Matches 55; Conservative 20; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 149; DB 1;
30.2%; Pred. No. 5.7e-08;
tive 20; Mismatches 57
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APPLICATION NUMBER: US/07/781,248A
FILING DATE: 19911230
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90103565
FILING DATE: 09-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07781248A Patent No. 5246699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ikeler, Barbara J. REGISTRATION NUMBER: 36,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 174 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal
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STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                            181 LP 182
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US-07-781-248A-1
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                                                                                                                                                                                                                                                             67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVMYH 126
                                                                                                                                                                                                                                                                                       9 OPVCRGGTQ--RPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
                                                                                                                                          24;
                                                                                               13.5%; Score 151; DB 4; Length 197; 25.0%; Pred. No. 4.2e-08; tive 26; Mismatches 64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Debre, Patrice
APPLICANT: Mossalayi, Mohammed D
TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
STREET: 556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B. Cells
CHO cells transformed with pCAL8-BF-ND
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/641,971B
FILING DATE: 19910116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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REGISTATION UNBER: 30258
REPERENCE/DOCKET NUMBER: 4-17921/+/DEB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              127 QPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS 158
                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90016254
FILING DATE: 24-JAN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/07641971B Patent No. 5236706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 174 amino acids TYPE: AMINO ACID
                                                                                               Query Match
Best Local Similarity 25.0%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908-277-4306
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
                                    ; ORGANISM: Homo sapien
US-09-602-877A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-
ORIGINAL SOURCE:
CELL TYPE: Hume
CELL LINE: CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-07-641-971B-1
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LENGTH: 197
TYPE: PRT
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57; Indels

Length 174;

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265 G----RWNDAFCDRKLGAWVC---DRLATCTPPASEGSAESMGPDSRPDPDGRLPTPS 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (515) 288-3667
TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 United States
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                            Des Moines
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                                                                                                                                     RESULT 11
US-08-365-103B-8
                                            181 LP 182
                                                                              316 AP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                        77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGI 134
                                                                                                 135 GGPYMFQWNDDRCNMK-NNFICKYSDEKPAV---PSREAEGE------ETELTTPV 180
                                                                                                                                                                    GGPYMFQWNDDRCNMK-NNFICKYSDEKPAV---PSREAEGE------ETELTTPV 180
                        77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 IGLRNLDLKGE------FIWVDGSHVDYSNWAPGEPTSRSQGEDCVMM-----RGS 264
17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                  US-08-365-103B-10

Sequence 10, Application US/08365103B

Sequence 10, Application US/08365103B

PRETEAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynch, Richard G

APPLICANT: Nunez, Raphael D.
APPLICANT: Yound, Jung!
TITLE OF INVENTION: DAN Sequences for Soluble Froms of CD23

TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET 801 Grand Ave. Suite 3200

CITY: Des Moines

STATE: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILLNG DATE: 28-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION UNBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf N5-24
TELECOMMUNICATION INFORMATION:
TELEFAX: (515) 288-367
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-365-103B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.2%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
                                                                                                                                                                                                                        181 LP 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 GGPYMFQWNDDRCNMK-NNFICKYSDEKPAV---PSREAEGE-----ETELTTPV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
Sequence 8, Application US/08365103B
Patent No. 5766943
GENERAL INFORMATION:
APPLICANT: Lynch, Richard G
APPLICANT: Wonez, Raphael D.
APPLICANT: Yodol, Jung1
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
13.4%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 1.3e-07;
Matches 55; Conservative 20; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCETAILING SISTEM: C. D.S./M.S. D.S. SCETARLE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INPOMMATION:
NAME: Mebel, Heidi S.
REGISTRATION NUMBER: 37,719
REGISTRATION NUMBER: Unff N5-24
TELECOMMULCATION: INFORMATION:
TELECOMMULCATION: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: patin Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAX-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-CCT-1991
PRIOR APPLICATION DATA:
APPLICATION UNDER: 181015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565D1C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08513278 Patent No. 5840844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 amino acids
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                      TYPE: PRT
ORGANISM: Homo saplens
US-09-517-605-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-513-278-4
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  SEQ ID NO 2
LENGTH: 404
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APPLICANT: Wown, Douglas S.
APPLICANT: Won Kooyk, Vette
APPLICANT: War Kooyk, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
FILE REFERENCE: 1049-1-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 SEDEQKLIEKFIENLLPSD-----GDFWIGLRRREEKQSNSTACQDLYAWT-DGSISQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 FRNWYVD-EPSCGSEVCVVM···YHQPSAPAGIGGPYMFQWNDDRCNMKNN-····FI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 YSNWHKELRNSCISKRCVSLLLDLSQPLLPNRLP----KWSEGPCGSPGSPGSNIEGFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LLSGQP------VCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LLLTQPGAGTGADTEAVVCVG---TACYTA----HSGKLSAAEAQNHCNQNGGNLATVK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,305
        GENERAL INFORMATION:
APPLICANT: Tenner et al., Andrea J.
TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT
NUMBER OF SEQUENCES: 33
CORRESSEE: Fish 6 Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 148.5;
24.4%; Pred. No. 3.9e
tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07306/012001
TELECOMMUTCATION INFORMATION:
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/751,305
18-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 CKYSDEKPAVPSREAEGEETELTTP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.4%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-751-305-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                              USA
Patent No. 5965439
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                92037
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                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-517-605-2
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                                                      Gaps
                                                                                                                              85 KQSNSTACQDLYAWTDGS--ISQFRN-WYVDEP-SCGSEVCVVMYHQPSAPAGIGGPYMF 140
                                                                                                                                                                                                                                            324 -----EGIWQWVDGSPLLPSFKQYWNRGEPNNVGEEDCAEF-----SGNG---- 363
                                                                                               25 YFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREE 84
                                                   Indels 41;
     Length 404;
                                                47;
DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: ROSEN, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
Ouery Match 13.0%; Score 144.5; DB 4 Best Local Similarity 29.7%; Pred. No. 5.3e-07; Matches 47; Conservative 23; Mismatches 47
                                                                                                                                                                                                                                                                                                   141 QWNDDRCNMKNNFICKYS-----DEK-----PAVPS 166
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                    85 KQSNSTACQDLYAW--TDGSIS-QFRNWYVDEPS--CGSEVCVVMYHQPSAPAGIGGPYM 139
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                                          Gaps
                                                                                             Gaps
                                                                      26 FHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLP-SDGDFWIGLRRREE 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
Query Match 12.9%; Score 143.5; DB 2; Length 372; Best Local Similarity 26.5%; Pred. No. 6e-07; Matches 41; Conservative 37; Mismatches 50; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 12.9%; Score 143.5; DB 6; Length 372; Best Local Similarity 26.5%; Pred. No. 6e-07; Matches 41; Conservative 37; Mismatches 50; Indels 27
                                                                                                                                                                                                                                                                                                                                              ant No. 5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
                                                                                                                                                                                                                    140 FQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 174
                                                                                                                                                                                                                                          140 FQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEET 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMUNOGLOBULING

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE: 21-JAN-1994

FILING DATE: 21-JAN-1994

FILING DATE: 10-DATA:

APPLICATION NUMBER: 986,931

FILING DATE: 16-DEC-1991

APPLICATION NUMBER: 440,625

FILING DATE: 16-DEC-1991

APPLICATION NUMBER: 315,015

FILING DATE: 22-NOV-1989

FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 20, 2003, 17:07:16
Job time : 17 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQ ID NO:4:
; LENGTH: 372
                                                                                                                                                                                                                                                                                                                                            ; Patent No.
                                                                                                                                                                                                                                                                                                             RESULT 15
5514582-4
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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: May 20, 2003, 17:06:10 ; Search time 56 Seconds
(without alignments)
364.814 Million cell updates/sec
1115
Sequence: US-09-887-855-5
Perfect score: 1115
Sequence: 1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 375593 seqs, 99172665 residues
Total number of hits satisfying chosen parameters: 375593
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries
Listing first 45 summaries

Published\_Applications\_AA:\*

| /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_|
| /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_|
| /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_|

Minimum DB seq length: 0 Maximum DB seq length: 200000000 ise : Published\_Applications\_AA:\*

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10: /cgn\_2\_6/ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\*

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12: /cgn\_2\_6/ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\*

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13: /cgn\_2\_6/ptodata/1/pubpaa/USO0\_NEW\_PUB.pep:\*

14: /cgn\_2\_6/ptodata/1/pubpaa/USO0\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Cuery

No. Score Match Length DB ID

1 1115 100:0 206 10 US-09-887-85-5 Sequence 15, Appli 2 110:0 206 10 US-09-887-855-2 Sequence 15, Appli 3 1115 100:0 374 9 US-10-149-819-15 Sequence 17, Appli 100:0 374 9 US-09-887-855-2 Sequence 137, Appli 382 9 US-09-907-824-137 Sequence 137, Appli 100:0 98.7 382 9 US-09-907-824-137 Sequence 137, Appli 100:0 98.7 382 9 US-09-907-844-137 Sequence 137, Appli 100:0 98.7 382 9 US-09-907-844-137 Sequence 137, Appli 100:0 98.7 382 9 US-09-907-844-137 Sequence 20, Appli 100:0 98.7 382 9 US-09-907-841-137 Sequence 20, Appli 100:0 98.7 382 9 US-10-176-758-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-176-758-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-175-737-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-175-738-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-175-738-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-175-738-20 Sequence 20, Appli 100:0 98.7 382 9 US-10-176-752-20 Sequence 20,

LPEETQEEDAKKTFKESREAALNLAY 206

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RESULT 2 US-10-149-819-15

Sequence 20, Appl Sequence 137, App Sequence 137, App Sequence 20, Appl Sequence 20,	Sagi	indels 0; Gaps 0;  RDGGQLVSIESEDEOKL 60
9 US-10-180-557-20 9 US-09-906-838-137 9 US-09-907-613-137 9 US-09-907-613-137 9 US-09-907-942-137 9 US-10-174-572-20 9 US-10-174-582-20 9 US-10-174-588-20 9 US-10-175-740-20 9 US-10-175-740-20 9 US-10-175-740-20 9 US-10-175-740-20 9 US-10-176-98-20 9 US-10-176-98-20 9 US-10-176-98-20 9 US-10-176-98-20 9 US-10-176-98-20 9 US-10-176-991-20 9 US-10-1776-993-20 9 US-10-177-993-20 9 US-10-177-993-20 9 US-10-177-993-20	ALIG 855 39 DNA 09/887 2	tch 100.0%; Score 1115; DB 10; Length 206; al Similarity 100.0%; Pred. No. 6.6e-103; 206; Conservative 0; Mismatches 0; Indels 0; G ATGRLLSGOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGOLVSIESEDEOKL
1101 98.7 382 1101 98.7 382	ALIG  TESULT 1  US-09-887-85-5  Sequence 5, Application US/09887855  Patent No. US2002058310A1  GENERAL INFORMATION: APPLICANT: Immunex Corporation APPLICANT: Immunex Corporation APPLICANT: LECTIN SS3939 DNA FILLE OF INVENTION: LECTIN SS3939 DNA FILLE OF INVENTION NUMBER: US/09/887  CURRENT FILING DATE: 2001-06-22  NUMBER OF SEQ ID NOS: 9  SEQ ID NO 5  LENGTH: 206  TYPE: PRT  ORGANISM: Home sapiens	rd C
	RESULT 1 US-09-887- ; Sequence ; Patent N ; GENERAL APPLICA ; APPLICA ; TITLE O ; FILE RE ; CURRENT ; CURRENT ; CURRENT ; SEQ ID N	Query M Best Lo Matches Qy 1 Db 1 Qy 61

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Matches 206; Conservative
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                                                                                                      APPLICANT: TANG, Y. Tom
APPLICANT: PATERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: BURCORD, Janice
APPLICANT: BURCORD, Mariah
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: PP-0760 PCT
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 06/172,852; 60/172,354
FRIOR ELING DATE: 1999-12-10; 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1115; DB 9; Length 374; Best Local Similarity 100.0%; Pred. No. 1.4e-102; Matches 206; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1
US-10-149-819-15
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GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Anderson, Dirk M
TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
FILE REFERENCE: 2883-US
CURRENT APPLICATION NUMBER: US/09/887,855
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
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Publication No. US20030044913A1
GENERAL INFORMATION:
                                                    APPLICANT: INCYTE GENOMICS, INC
APPLICANT: YUE, Henry
APPLICANT: AZIMZAI, Yalda
APPLICANT: TANG, Y. TOM
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100.0%;
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SOFTWARE: PERL Program
SEQ ID NO 15
LENGTH: 374
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; LENGTH: 374
: TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-855-2
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Best Local Similarity
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-09-887-855-2
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ITLE OF INVENTION: Secreted

ITLE OF INVENTION: Secreted

ITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR PELICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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                                                                                                                                                                       Gaps
                                             1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60
                                                                            22 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 81
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  Indels
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  Mismatches
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/28214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 137, Application US/09905291A Patent No. US20020160374A1
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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; ORGANISM: Homo Sapten
US-09-902-853-137
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US-09-907-824-137
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                         98.7%; Score 1101; DB 9; Length 382; 96.3%; Pred. No. 3.6e-101;
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0; Mismatches
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
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Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Wood, William, I.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
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Matches 206; Conservative
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Eaton, Dan L.
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                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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98.7%; Score 1101; DB 9;
Best Local Similarity 96.3%; Pred. No. 3.6e-101;
Matches 206; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PRICATION NUMBER: PCT/US99/30999
PRIOR PRILING DATE: 1999-12-20
PRIOR PRILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
                                                                                                             CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PLILING DATE: 1099-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-09-08
PRIOR PELING DATE: 1999-09-08
                                  TITLE OF INVENTION: Acids Encoding the S:
THE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
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PRIOR FILING DATE: 1999-11-29
PRIOR PLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-05
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; Publication No. US20020197671A1
; GENERAL INFORMATION:
    APPLICANT: Genentech, Inc.
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PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLIING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
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PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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PRIOR FILING DATE: 1999-10-05
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Kljavin, Ivar J.
Mather, Jennie P.
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                                               Desnoyers, Luc
Eaton, Dan L.
Ashkenazi, Avi
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US-09-907-824-137
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APPLICANT
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Length 382;

DB 9;

98.7%; Score 1101;

Query Match

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TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR PRICE APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
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PRIOR PILING DATE: 1999-07-28
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                                                                1 ATGRILS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
                                                                                       22 ATGRILISASDLDLRGGQPVCRGGTQRPCYKVIYFHD1FSRRLNFEEAKEACRRDGGQLVSI 81
                         Gaps
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                       Indels
Best Local Similarity 96.3%; Pred. No. 3.6e-101; Matches 206; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: PCT/US99/21090
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PELLING DATE: 1999-07-28
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-09-15
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FILING DATE: 1999-10-05
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Grimaldi, Christopher J.
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Wood, William, I.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Botstein, David
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Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/09/904,011

PRIOR PELLING DATE: 2001-07-11

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: PCT/US00/0414

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
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Best Local Similarity 96.3%; Pred. No. 3.6e-101;
Matches 206; Conservative 0; Mismatches 0;
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Publication No. US20030003530A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-907-841-137
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Best Local Similarity
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53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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Pred. No. 3.6e-101;
0; Mismatches 0;
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PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30919
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 382
                                                                                                                                                                                                                                                           FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
                                                                     APPLICATION NUMBER: PCT/US99/20594
FILING DAFE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/21090
60/146,222
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Best Local Similarity 96.3%;
Matches 206; Conservative
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William I.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gundey, Austin L
APPLICANT: Sunth, Victoria
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Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-137
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US-10-174-590-20
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APPLICANT:
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ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 141
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                                                                                                                                                                                                                                                            ; Sequence 20, Application US/10175737; Publication No. US20030013153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.7
Best Local Similarity 96.3
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-20
                                                                                                                                                                                                                                                                                                                                              Chen, Jian
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Abang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT APPLICATION FEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 193430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
LENGTH: 382
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                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                      1 ATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
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                                                                                                                                                                                                                                                       Score 1101; DB 9;
Pred. No. 3.6e-101;
0; Mismatches 0;
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Publication No. US20030008353A1
GENERAL INFORMATION:
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Best Local Similarity 96.3%;
Matches 206; Conservative
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                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-20
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US-10-176-758-20
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APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: SEGNET DAID TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1650
CURRENT APPLICATION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1650
CURRENT APPLICATION: D67105
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
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113 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE
                             22 ATGRILISASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
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96.3%; Pred. No. 3.6e-101;
ive 0; Mismatches 0;
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                                                                                           173 ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
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## APPLICANT: Williams, P. Mickey
## APPLICANT: Williams, P. Mickey
## APPLICANT: Williams, P. Mickey
## APPLICANT: Word, William, I.
## TTTLE OF INVERTION: Secreted and Transmembrane Polypeptides and Nucleic
## TTTLE OF INVERTION: Acids Encoding the Same
## TTTLE OF TILKE OATE: 2000-09-16
## PRIOR FILIKE OATE: 2000-09-16
## PRIOR PELICATION NUMBER: US 60/145,698
## PRIOR FILIKE OATE: 1999-07-26
## PRIOR FILIKE OATE: 1999-07-28
## PRIOR FILIKE OATE: 1999-09-13
## PRIOR FILIKE OATE: 1999-01-36
## PRIOR FILIKE OATE: 1999-01-36
## PRIOR FILIKE OATE: 1999-11-30
## PRIOR FILIKE OATE: 1999-11-30
## PRIOR FILIKE OATE: 1999-11-20
## PRIOR FILIKE OATE: 1999-11-30
## PRIO
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Pred. No. 3.6e-101;
0; Mismatches 0;
                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                           Pan, James
Paoni, Nicholas F.
                                                                               Gerritsen, Mary E. Goddard, A.
                                                                                                                                                                                                                                       Kljavin, Ivar J.
Mather, Jennie P.
                                                            Gerber, Hanspeter
Fong, Snerm
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Best Local S
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R10: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R10: US/10/173,706
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
FILE REPERENCE: P3450R10: ACID NUMBER: US/10/173,706
CURRENT PILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 612
ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
                   EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                                                           142 EPSCGSEVCVVMYHQPSAPAGIGGPYMFQMNDDRCNMKNNFICKYSDEKPAVPSREAEGE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVD 112
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Pred. No. 3.6e-101;
0; Mismatches 0;
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Publication No. US20030022293A1
GENERAL INFORMATION:
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Best Local Similarity 96.3%;
Matches 206; Conservative
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Watanabe, Colin K.
Wood, William I.
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
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US-10-173-706-20
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Apply, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175, 738
CURRENT FILING DATE: 2002-06-19
PRIOR application removed - See File Wrapper or Palm
NUMBER OF SO ID NOS: 612
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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APPLICANT: Character Secretary
APPLICANT: Character APJ 30 RIC60
CURRENT APPLICATION NUMBER: US/10/175, 752
CURRENT APPLICATION NUMBER: US/10/175, 752
CURRENT FILING DATE: 2002-06-19
Prior APPLICATION NUMBER: See File Wrapper or Palm
SEO ID NOS: 612
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Pred. No. 3.6e-101;
0; Mismatches 0; Indels
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96.3%; Pred. No. 3.6e-101;
tive 0; Mismatches 0;
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Publication No. US20030022295A1
GENERAL INFORMATION:
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Best Local Similarity 96.3%;
Matches 206; Conservative
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US-10-175-738-20
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US-10-175-752-20
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LENGTH: 382
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EPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGE 172
                                                                                                              22 ATGRILISASDLDLRGGQPVCRGGTQRPCYKVIYFHDITSRRLNFEEAKEACRRDGGQLVSI
1 ATGRLLS------GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI
                                                                                                                                                               ETELTTPVLPEETQEEDAKKTFKESREAALNLAY 206
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 20, 2003, 17:03:25 ; Search time 44 Seconds (without alignments) 450.084 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-887-855-5 1115 1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	mannose recentor o		TOTAL TOTAL	ç					+	mannose receptor.	Droteoglycan core	addregan - howine		E-Selectin precure	proteoglycan core	brevican precureor	hypothetical prote	IGE For recentor it	brevican - buman /	addredan negarior	protein F52E1 2 11	brevican precursor	lectin BRA3-1 prec	addregan pregran	SCAVENGET PERFORM	hrevican precureor	Jectin - harnacle		HIV gp120-binding
SUMMAKIES	£		A36563	A48925	S52781	T14274	T42389	S28764	A55535	A60979	A47171	T42710	A39808	T42630	A39086	B42755	A28452	A54423	T24425	LNHUER	T46256	A55182	E89130	S57653	LNRC1	150421	JC7595	S49126	S10548	\$23936	A46274
	ond th	match bength bb	1456 1	'n														912 2					253 2						173 2	372 2	404 2
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coaqulation factor	L-selectin precurs	hypothetical prote	bitiscetin alpha c	phospholipase-A(2)	IqE Fc receptor, 1	lectin BRA3-2 prec	L-selectin precurs	pulmonary surfacta	pulmonary surfacta	pulmonary surfacta	lectin precursor -	coaqulation factor	tetranectin precur	hypothetical prote	19E Fc receptor II
JC4329	A32375	T26655	JC5058	S48719	LUMSER	LNRC3	S22124	LNHUPS	LNHUP6	LNHUP1	LNFHLS	JC4690	JC4031	T29200	S34198
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129 2	372 1	463	131	1487	331	162	370	248	248 1	248 1	283 1	152 2	202 2	280 2	309
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#### ALIGNMENTS

RESULT 1

	A36563 _
	mannose receptor precursor - human
	C;Species: Homo sapiens (man)
	C; Accession: A36563; A60926; A44255; B44255; C44255; D44255; E44255; F44255; G44255
_	KTYBYLOR, M.E.; CONATY, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K. J. Biol Chem 245 12156-12162 1000
	A:Title: Primary structure of the mannose recentor contains multiple motife recemb
	A; Reference number: A36563; MUID:90324192; PMID:2373685
	A; Accession: A36563
	A Molecule type: mrw A Posidings 1-1456 /mrv
	A.Cross-references: GB.305550; NID:q188675; PIDN:AAA59868.1: PID:q188676
	A, Note: parts of this sequence, including the amino end of the mature protein, were
_	R;Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A. J. Exp. Med 172 1785-1764 1990
•	A.Title: Molecular characterization of the human macrophage mannose recentor. demon-
	A; Reference number: A60926; MUID:91079783; PMID:2258707
	A;Accession: A60926
	A;Status: nucleic acid sequence not shown
	A: Molecule - Vype: MRNA A: Dociding: 1-1332 /m/ 1335 1165 / mms.
	A. NESTULUES: 1 - 1.337 T. J. 1.350 AEZEV
_	A:\.Uofe: translation of the nucleotide commence is incomplete.
_	A.NOCE: in the authors' translation additional residues Pro-Glu-Ile are shown after
	R;Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
_	Genomics 14, 721-727, 1992
_	A, Title: Organization of the gene encoding the human macrophage mannose receptor (M)
	A.Kererence number: A44255; MUID:93052405; PMID:1294118
	A) Arterosauli Adda20 A) Statesauli interest our los acid common act about 1
	A: Social First NAT First NAT Conceptual Sequence not snown; not compared with conceptual
	A. Residues: 155-233, KSAL', 238-283:346-428:492-569-631-714-716-719-783-80-1
	A; Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:1118421, NCBIP:1118
	C:Genetics:
_	A Gene GDB:WRC1
_	A:Map bostion: 10ml-10ml3
_	C; Superfamily: phospholipase A2 receptor: C-type lectin homology: fibronectin type
	C; Keywords: duplication; lectin; tandem repeat; transmembrane protein
	F;1-18/Domain: signal sequence #status predicted <sig></sig>
	F:166-209/Domain: fibronectin type II repeat homology <2F1>
	F;zz3-340/bomain: C-type lectin homology <lch1></lch1>
	F;30Z-48b/Domain: C-type lectin homology <lch2> F;345-1079/Domain: C-type lectin homology <lch3></lch3></lch2>
	Ouery Match 16 3%. Soore 182. DR 1. fameth 1456.
	Similarity 25.5%; Pred. No. 9.3e-08;
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	QY 188EDAKKTFKESREAALNL 204 :   ::::: :  Db 954 CFKIFGFANEEKKSWQDARQACKGL 978
139 MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPEETQE	RESULT 3 S52781 neurocan - mouse C; Species: Mus musculus (house mouse)
Qy 188EDAKKTFKESREAAL 202  :: : : :   55 KCFKIFGFMEERKKWQEARKACI 978	C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000 C;Accession: S52781 R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R. aubmitted to the EMBL Data Library February 1995 A;Description: Anino Acid sequence of money needs and breview and their different
RESULT 2 A48925 mannose receptor precursor, macrophage - mouse	A; Reference number: S52781 A; Accession: S52781 A; Status: preliminary A; Molecule type: mRNA
C:59Ec1es: mus musculus (nouse mouse) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C:Accession: A48925; S21320; PC2245 R:Harris, N: Super, M: Rits, M.; Chang, G.; Ezekowitz, R.A. Blood 80, 2363-2373, 1992	A; Residues: 1-1268 <rau> A; Residues: EMBL:X84727; NID:9758629; PIDN:CAA59216.1; PID:9758630 A; Cross:references: EMBL:X84727; NID:9758629; PIDN:CAA59216.1; PID:9758630 C; Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: link protein repeat homology <lnk1> E; 176-253 / Domain: li</lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></lnk1></rau>
A;Title: Characterization of the murine macrophage mannose receptor: demonstration that A;Reference number: A48925; MUID:93043353; PMID:1421407 A;Accession: A48925 A;Accession: A48925 A;Status: not compared with conceptual translation	F:248-25/Domain: int protein repeat nomotogy <pre>c.248-25/Domain: EdF homology <pre>c.264-995/Domain: EdF homology <pre>c.26F&gt; F:1040-1160/Domain: C-type lectin homology <lch> F:1167-1223/Domain: complement factor H repeat homology <fhd></fhd></lch></pre></pre></pre>
A; Molecule type: mRNA A; Residues: 1-1455 <har> A; Experimental source: peritoneal macrophage A: Mote. sources peritoned from WrbI hackbook WrbII. 110733</har>	Query Match 15.9%; Score 177; DB 2; Length 1268; Best Local Similarity 31.5%; Pred. No. 2.2e-07; Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;
R.Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.B. submitted to the EMBL Data Library, April 1992 A; Description: Characterization of the murine macrophage mannose receptor: Demonstration	<u> </u>
On. A. Reference number: S21320 A. Accession: S21320 A. Status: preliminary	
A;Residues: 1-302, W. 303-1117, E',1119-1455 <ha2> A;Residues: 1-302, W. 303-1117, E',1119-1455 <ha2> A;Cross-references: EMBL:Z11974; NID:952997; PIDN:CAA78028.1; PID:952998 R;Harris, N.; Peters, L.L.; Elcher, E.M.; Rits, M.; Raspberry, D.; Elchbaum, Q.G.; Super</ha2></ha2>	
crol	4
	T14274 versican precursor, splice form V2 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
A; Map position: 2 C; Superfamily: phospholipase A2 receptor; C·type lectin homology; fibronectin type II re C; Keywords: membrane protein; receptor F; 168-209/Domain: fibronectin type II repeat homology <2F9> F; 361-485/Domain: C-type lectin homology <lch1> F; 943-1077/Domain: C-type lectin homology <lch2></lch2></lch1>	C:Accession: T14274 R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R. J. Biol. Chem. 273, 15758-15764, 1998 A;Title: Versican v2 is a major extracellular matrix component of the mature bovine A;Reference number: 217954; MUID:98288320; PMID:9624174 A;Accession: T14274 A;Accession: T14274
	A; Molecule type: mRNA A; Residues: 1-1643 <sch> A; Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1 A; Experimental source: brain</sch>
OY 21 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR 80	C;Reywords: glycoprotein F;1-20/Domain: signal sequence #status predicted <sig> F;1-1643/Product: versican, splice form V2 #status predicted <mat> F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent)</mat></sig>
OY 81 RREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGSEVCVVWYHQPSAPAGIGGPY 138 : :	Query Match 15.7%; Score 174.5; DB 2; Length 1643; Best Local Similarity 25.5%; Pred. No. 4.9e-07; Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
Qy 139 MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVLPEETQE 187	KLIEKFIENLLPSDGDF- 75 ::

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49;
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                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 4e-07; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Contains: glial hyaluronate-binding protein
                                                                                                                                                                                                                                                                                                          15.6%; Score 174;
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-----RWNDVPCNYNLPYVCK 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 IGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.8%;
Matches 44; Conservative 1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                             Versian precursor, splice form VO - bowine
N'Alternate names: chondroitin sulfate proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C;Accession: T42389
R;Schadifeldt, M.; Dours-2immermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bowine brain A;Reference number: 217954; MUID:98288320; PMID:9624174
A;Accession: T42389
A;Atcession: T42389
A;Atcession: T42389
A;Accession: T42389
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T42380
A;Retus: preliminary
A;Accession: T42380
A;Retus: preliminary
A;Accession: T42380
A;Retus: preliminary
A;Coss-references: EMBL:AF060456; NID:93253299; PID:932533300; PIDN:AAC24358 J
C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin C;Keywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F;1-20/Domain: signal sequence #status predicted <MAT>
F;21-3381/Product: versican, splice form V0 #status predicted <MAT>
F;57,331,332,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2269,2356,28
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: 22 Nov. 1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C; Accession: 528764
R; Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
R; Rauch, Chem. 267, 19536-19547, 1992
A; Title: Cloning and primary structure of neurocan, a developmentally regulated, aggree_A; Reference number: $28764, MUID:92406907; PMID:1326557
A; Accession: $28764
A; Moclecule type: mRNA
A; Rosidues: 1-1257 < RAU>
A; Rosidues: 1-1257 < RAU>
A; Cross-references: EMBL:M97161; NID:9205649; PIDN:AAC37679.1; PID:9205650
C; Superfamily: aggreean: C-type lectin homology; complement factor H repeat homology; IC; Superfamily: aggreean: C-type lectin homology; glycoprotein
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                                                                                                                                                  1522 -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----OWNDVPCNYHLTYTCKKGTVACGOPPVVENAKTFGKMKPRYEINSLIRYHC 3310
76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
                                                   1472 WIGL------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSTGEDCVVIIWHENG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 WIGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 15.7%; Score 174.5; DB 2; Length 3381; 1 Similarity 25.5%; Pred. No. 1.1e-06; 59; Conservative 26; Mismatches 71; Indels 75;
                                                                                                                                                                                                                                                                     1573 KDGFIQRHLPTIRCLGNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ETELTT------PVL---PEETQEEDAKKTFKESREAALN
                                                                                                                                                                                                                    173 ----ETELTT------PVL----PEETQEEDAKKTFKESREAALN
                                                                                                          132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE----
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C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
A; Itol: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan gen. A; Reference number: A5535
A; Reference number: A5535, MUD: 9512551; PMID: 7822336
A; Recession: A5535
A; Residues: 1-2397 <RES>
A; Molecule type: mRNA
A; Residues: 1-2397 <RES>
A; Cross-references: GB:D16263; NID: 9862460; PIDN: BAA0,796.1; PID: 9862461
C; Superfamily: versican; C-type lectin homology; complement factor H repeat homology
E; 1-20/Domain: signal sequence #status predicted <ARA>
F; 21-1654/Domain: EGF homology <ARA>
F; 2095-2126/Domain: EGF homology <EDS>
F; 2131-2291/Domain: EGF homology <EGS>
F; 2131-2291/Domain: C-type lectin homology <LCH>
F; 2171-2291/Domain: C-type lectin homology <LCH>
F; 2171-2201/Domain: C-type lectin homology <LCH>
F; 2171-2291/Domain: C-type lectin homology <LCH>
F; 2171-2291/Domain: C-type lectin homology <LCH>
F; 2171-2291/Domain: C-type lectin homology <LCH>
F; 2171-2201/Domain: C-type lectin homology
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                                                                                                                                                                                                                                                        IGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 133
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                                                                                                                                          17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
F:23-1257/Product: neurocan #status predicted <MAT>
F:23-1257/Product: neurocan #status predicted <MAT>
F:176-253/Domain: link protein repeat homology <LNK1>
F:274-355/Domain: link protein repeat homology <LNK2>
F:364-366/Region: cell attachment (R-G-D) motif
F:953-984/Domain: Cell performent (R-G-D) motif
F:953-984/Domain: Cetype lectin homology <LCH>
F:1156-1137/Domain: complement factor H repeat homology <FHD>
F:1156-1212/Domain: complement factor H repeat homology <FHD>
F:121,339,737,967,1164/Reinding site: carbohydrate (Asn) (covalent) #site: R:372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status in the constant of the covalent of the covalent
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F;2298-2354/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 2312
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Gaps

55;

Length 2409;

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chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J; Blol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed du
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A;Accession: A47171
A;Status: preliminary
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3562 cSHID
A;Cross-references: GB:D13542; NID:9391643; PIDN:BAA02742.1; PID:9391644
A;Cross-references: GB:D13542; NID:9391643; PIDN:BAA02742.1; PID:9391644
A;Experimental source: stage 22-23 developing limb buds
A;Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superifamily: chicken chondroitin sulfate proteogyycan PG-M core protein; C-type le
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-345/Domain: link protein repeat homology <LNK2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2190 QGQCIK--YF---AHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRV------GHDYQ 2237
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mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: l1-Jan-2000 #sequence_revision l1-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2338 WIGE------NDKMFEHDFRWTDGSTLQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroliin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
F;2142-2137/Domain: C-type lectin homology <LCH>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2182-2305/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------QWNDVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 3475
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                                                                                                                                                                                                                                                                                                                         15.6%; Score 174; DB 1;
28.5%; Pred. No. 8.5e-07;
1ve 23; Mismatches 55
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F;3296-3327/Domain: EGF homology <EGF>
F;3334-3454/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.58
Matches 47; Conservative
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Matches 4
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A.Accession: S06014
A.Nolecule type: mRNA
A.Residues: 1-2409 <2IMA
A.Cross-references: GB:X15998; NID:g37662; PIDN:CAA34128.1; PID:g37663
R.Yao, L.Y.; Moddy, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A.Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by A.Recession: S43921; MUID:95005762; PMID:7921538
A.Recession: S43921; MUID:95005762; PMID:7921538
A.Residues: 208-440;1094-1385;1910-2246 <7AO>
R.Residues: 208-440;1094-1385;1910-2246 <7AO>
R.Residues: 208-440;1094-1385;1910-2246 <AO>
Brain Res. Bull: 22, 67-70, 1989
A.Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A.Reference number: A60979; MUID:89229983; PMID:2469524
A.Recession: A60979;
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A; Mestdues: 21-22, 'X', 24-37 < PE2>
A; Residues: 21-22, 'X', 24-37 < PE2>
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:118884)
B; Nozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics: 14, 845-851, 1992
A; Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chrc
A; Reference number: 154179; MUID:93122792; PMID:1478664
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A;Cross-references: GDB:127873; OMIM:118661
A;Map position: Sq12-Sq14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology;
E;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>
                                                                                                                                                                                                                  N; Contains: glial hyaluronate-bidding protein
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 10-Sep-1999 *text_change 19-Jan-2001
C; Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R; Zimmermann, D. R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A; Title: Multiple domains of the large fibroblast proteoglycan, versican.
A; Reference number: S06014; MulD: 90059882; PMID: 2583089
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A; Residues: 1725, 'V', 1727-2409 <KRU>
A; Residues: 1725, 'V', 1727-2409 <KRU>
A; Cross: references: GB-102814
B; Perides, G.; Rahemtulla, F; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A; Title: Isolation of a large aggregating proteoglycan from human brain.
A; Reference number: A45131; MUID:93054756; PMID:1429726
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A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:g263313; PIDN:AAB24878.1; PID:g263314
                                                                                                                               versican precursor - human
N:Alternate names: chondroitin sulfate proteoglycan 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
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8;

Length 3562; 55; Indels

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A; Molecule type: protein
A; Residues: 1230-1249 <PE2>
C; Superfamily: agreean; C-type lectin homology; complement factor H repeat homolog
C; Keywords: glycoprotein
C; Keywords: glycoprotein
E; 8-28/Domain: link protein repeat homology (fragment) <LNK1>
F; 80-146/Domain: link protein repeat homology (fragments) <LNK3>
F; 80-146/Domain: link protein repeat homology (fragments) <LNK3>
F; 1130-1250/Domain: C-type lectin homology <LCH>
F; 11257-1313/Domain: C-type lectin homology <LCH>
F; 11257-1313/Domain: Complement factor H repeat homology <FHD>
              A; Reference number: A91327; MUID:85027710; PMID:6489519
A;Accession: E29164
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A39086
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No.Alternate names: aggreene: aggreening cartilage protecoglycan
C.Species: Bos prinigenius taurus (cattie)
C.Species: Dos prinigenius taurus (cattie)
C.Species: 20.*Nar-1922 sequence_revision 23.*Nar-1955 *text_change 13.*Aug-1999
C.Accession: A34224; A27752; A3989; A27751; E29164; B27751; C27751; D27751; E27751; E27751
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A;Residues: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomen
C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
B;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21333-21336.
A;Title: Characterization of a novel member of the macrophage mannose receptor type C A;Reference number: Z22235; MUID:9635501; PMID:8702911
A;Accession: T42710
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1479 <WUK>
A;Residues: 1-1479 <WUK>
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 170.5; DB 2.31.4%; Pred. No. 9.8e-07; tive 22; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | | | :| || || || || IW----GPEG------RWNDSPCNQSLPSICK 504
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nes 48; Conservative
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Matches
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A Accession: T42636
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: 1-233 RHBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Accession: T42630
R.Hering, T.M.; Kollar, J.; Huynh, T.D.
R.Herence number: 222182
R.Reference number: 222182
                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                  C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ENLLPSDGDF-WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227 VVMIWHEKG------EWNDVPCNYQLPFTCKKGTVACGEPPVVEHARIFGOKKD 1274
                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                         9 QPVCRGG---TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
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                                                                                                                                                  43;
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                                                                                                                                                  Indels
                                                                                                                                           59;
                   Score 158.5; DB 2;
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Query Match 14.2%; Score 158.5; DB Best Local Similarity 26.8%; Pred. No. 1e-05; Matches 48; Conservative 29; Mismatches :
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A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
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                                        S66389; S68646; S62786; A34226; B43919; C43
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A; Residues: 764-765, A', 767-846, 'V', 848-862, 'X', 864 < BAR>
A; Cross-references: EMBL:S74659: NID:9807127; PIDN:AAC60643.1; PID:9807128
A; Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue R; Ilic, M.Z.; MOK, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J. Arch. Blochem. Blochem. Biophys. 322, 230, 1995
A; Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the A; Reference number: S66389; MUID:96004775; PMID:7574678
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A; Molecule type: protein
A; Molecule type: protein
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A. Residues: 1-2162,2201-2329,'A',2392-2415 <a href="https://documents.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile.com/mile
C; Accession: A39086; S50206; A43919; S46559; S66389; S68646; S62786; A34226; B43919; C4 R; Doege, K.J.; Sasaki, M.; Kinura, T.; Yamada, Y. Biol. Chem. 266, 894-902, 1991
A; Title: Complete coding sequence and deduced primary structure of the human cartilage A; Reference number: A39086; MUID: 91093289; PMID: 1985970
A; Recassion: A39086
A; Status: preliminary
A; Molecule type: mRNA
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J. Biol. Chem. 264, 15747-15750, 1989
A:Title: A new epidermal growth factor-like domain in the human core protein for the A;Reference number: A34226; MUID:89380154; PMID:2789216
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A;Residues: 1778-1927,'A',1929-1963,'V',1965-2162,2201-2415 <DUD>
A;Cross-references: EMBL:X17406; NID:930248; PIDN:CAA35463.1; PID:930249
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1990
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A; Molecule type: protein
A; Residues: 17-23; 24, 'X', 26-27; 393-401; 402-403 < LLI>
R; Residues: 17-23; 24, 'X', Knaeuper, 'V.; Murphy, G.; Neame, P.J.
R; Fosang, A.J.; Last, K.; Knaeuper, 'V.; Murphy, G.; Neame, P.J.
A; FEBS Lett. 380, 17-20, 1996
A; Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A; Reference number: S68646; MUID:96181659; PMID:8603731
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 361-370, X', 372-373; 393-399, 'X', 401-407, 'X', 409 <SAN>
A; Cross-references: PION: ABB22079_1; PID: 9248844; PIDN: AAB22077_1;
A; Experimental source: synovial fluid
A; Experimental source: synovial fluid
A; Experimental source: synovial fluid
A; Barry, F. P.; Neame, P. J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A; Title: Length variation in the keratan sulfate domain of mammalian
A; Reference number: 146998; MUID: 95128522; PMID: 7827755
A; Accession: $46659
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A;Residues: 1936-1963,'V',1965-2069,'A',2071-2415
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A. Gene: GDB:AGC1; CSPG1; CSPGCP; MSK16
A. Gene: GDB:AGC1; CSPG1; CSPGCP; MSK16
A. Gene: GDB:AGC1; CSPG1; CSPGCP; MKH155760
A. Map position: 1546-1546
C. Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology
C. Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extra
F. 19. 19. Domain: signal sequence * **status predicted < **SiG2**
F. 20-2162,2201-2415/Product: aggrecan cartilage short splice form **status predicted F: 20-2162,2201-2329, **A. / 2392-2415/Product: aggrecan short splice form **status predicted F: 20-2162,2201-2329, **A. / 2392-2415/Product: aggrecan short splice form **status predicted F: 24-115/Domain: link protein repeat homology < LNK3>
F: 24-115/Domain: link protein repeat homology < LNK3>
F: 3495-572/Domain: link protein repeat homology < LNK3>
F: 593-673/Domain: link protein repeat homology < LNK3>
F: 593-673/Domain: chondroitin sulfate attachment **status predicted < CS2>
F: 1511-2162/Domain: chondroitin sulfate attachment **status predicted < CS2>
F: 1511-2205-2325/Domain: C-type lectin homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2205-2325/Domain: complement factor H repeat homology < LNK5>
F: 2312-2325/Domain: complement factor H repeat homology < LNK5>
F: 2312-2325/Domain: complement factor H repeat homology < LNK5>
F: 2313-2333, 387, 434, 602, 657, 737, 1898/Buiding site: carbohydrate (Asn) (covalent) *
F: 3311, 376/Buiding site: keratan sulfate (Thr) (covalent) **
F: 3311, 376/Buiding site: keratan sulfate (Thr) (covalent) **
F: 3311, 376/Buiding site: keratan sulfate (Thr) (covalent) **
F: 3311, 376/Buiding site: keratan sulfate (Thr) (covalent) **
F: 3312-3411, 376/Buiding site: Keratan sulfate (Thr) (covalent) **
F: 3411, 371, 371,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
B42755
E-selectin precursor - mouse
N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: 232174, and Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J
Eur. J. Blochem. 206, 401-411, 1992
A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and A;Reference number: S23174
A;Accession: S23174
A;Accession: S23174
A;Accession: S23174
A;Accession: S23174
A;Molecule type: DNA
A;Residues: 1-612 <ABC>
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
B;Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-sel
A;Accession: D. 2775
A;Accession: D. 27755; MUID:92340571; PMID:1378846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 'MKATAGV', 1-389,391-612 <WELD.
A; Cross-references: GB:M87862; NID:g193107
A; Cross-references: GB:M87862; NID:g193107
A; Experimental source: endothelial cells
A; Experimental source: endothelial cells
A; Note: sequence extracted from NEB backbone (NCBIP:109470)
A; Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PI
A; Note: it is uncertain whether the initiator is Met-1 or the AuG codon preceding th C; Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homolo C; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%; Score 158.5; DB 29.1%; Pred. No. 2e-05; iive 22; Mismatches 6
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ses 52; Conserv
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us-09-887-855-5.rpr

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proteoglycan core protein precursor, cartilage - rat
N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A28453; A28452
R;Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J BIOL. Chem. 252, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduct A;Reference number: A92623; MUID:88087070; PMID:3693370
A;Accession: A92623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA Apples mRNA Apples mRNA Apples mRNA Apples mRNA Apples mRNA Apples 1856-2124 AD02> A; Residues: 1856-2124 BH13518; NID:9206104; PIDN:AAA41836.1; PID:9206105 B; Neame, P.J.; Christner, J.E.; Baker, J.R. B. Bloot. Chem. 252, 17768-1778, 1987 A; Title: Cartilage proteodlycan aggregates. The link protein and proteoglycan amino-term A; Reference number: A28453; MUID:88087071; PMID:3693371
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A;Molecule type: protein
A;Residues: 20-37, W/,39-60, E',62-64, X',66-69;70-83;84,89-148, L',150-238, 'S',240,'A'
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; E;
C;Keywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: mRNA
A.Residues: 1-2124 <DOE>
A.Residues: 1-2124 <DOE>
A.Residues: 1-2124 <DOE>
B. Frobege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
A;Reference number: annotation; revision to residue 698
B;Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat
A;Reference number: A23835; MUID:86250698; PMID:2424893
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: P-selectin #status predicted <MAT>
F;22-612/Product: P-selectin #status predicted <MAT>
F;143-174/Domain: EGF homology <EGF>
F;140-238/Domain: Complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;365-363/Domain: complement factor H repeat homology <FH3>
F;368-426/Domain: complement factor H repeat homology <FH4>
F;31-489/Domain: complement factor H repeat homology <FH6>
F;341-489/Domain: complement factor H repeat homology <FH6>
F;35,391,528/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 KOSNSTACODLYAWIDGS---ISQFRNWYVDEPS--CGSEVCVVMYHQPSAPAGIGGPYM 139
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F;44-135/Domain: immunoglobulin homology <IMM>
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13.9%; Score 154.5; DB 2; Length 6
Best Local Similarity 27.9%; Pred. No. 9.2e-06;
Matches 38; Conservative 28; Mismatches 45; Indels
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F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;612-683/Domain: C-type lectin homology <LOK4>
F;1914-2034/Domain: C-type lectin homology <LOK4>
F;2041-2097/Domain: complement factor H repeat homology <FHD>
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Search completed: May 20, 2003, 17:06:57 Job time: 48 secs

## GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 20, 2003, 17:00:15 ; Search time 13 Seconds (without alignments) 657.240 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-887-855-5 1115 1 ATGRLLSGQPVCRGGTQRPC......EEDAKKTFKESREAALNLAY 206

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description		Q9cxm0 mus musculu	Q9h9p2 homo sapien	P22897 homo sapien	mus m	pos	ratt	rattus	Q62059 mus musculu		_	rattus	P13608 bos taurus	P16112 homo sapien	_	_	O89103 mus musculu	P07897 rattus norv	Q28062 bos taurus	Q9npy3 homo sapien	homo	рошо	mus m		-	Q9ygp1 trimeresuru	P55068 rattus norv	Š	P30836 rattus norv	_	mus	5 ratt	39	13
DI		CHOD_MOUSE	CHOD_HUMAN	MANR_HUMAN	PGCN_MOUSE	PGCV_BOVIN	PGCN_RAT	PGCV_RAT	PGCV_MOUSE	PGCV_HUMAN	PGCV_CHICK	CD93_RAT	PGCA_BOVIN	PGCA_HUMAN	PGCA_CANFA	LEM2_MOUSE	CD93_MOUSE	PGCA_RAT	PGCB_BOVIN	CD93_HUMAN	CLF1_HUMAN	FCE2_HUMAN	PGCA_MOUSE	PGCB_MOUSE	PGCA_CHICK	LECG_TRIST	PGCB_RAT	LEC2_MEGRO	LEM1_RAT	LEM1_MOUSE	FCE2_MOUSE	LEM2_RAT	LEC3_MEGRO	LEM1_BOVIN
DB	1	7	٦,	٠,	٦.	-	-	-	<b>-</b>		н.	-	<b>.</b>		-	Η.	-	<b>~</b>	۰,	٠,	н,	н,	٠,	٦,	٠,	٠,	۰,	<b>.</b>	-	-	-	-		-
% Query Match Length		273	273	1456	1268	3381	1257	2738	3358	3396	3562	643	2364	2415	2333	612	644	2124	912	652	197	321	2132	883	2109	PCT	883	173	372	372	331	249	162	370
% Query Match			50.4		15.9		15.6			٠	'n.	÷.	٠	4.	<u>.</u>	13.9			13.6				•	13.2				٠.	÷	'n	ς.	٠	'n	12.6
Score		574	561.5	182	1/1	174.5	174	174	174	174	171	165	200	158.5	155.5	154.5	153.5	153.5	٦;	151.5	151	٦,	148.5	147	0 1 7	n t	٦;	4	44	43	41	;	<b>6</b>	140
Result No.		٦,	7 (	η.	er i	'n	9	7	<b>3</b> 0 (	د د	01:	<b>1</b> :	12	÷ ;	14	15	91	17	20 0	<b>→</b> (	2 5	77	77	52	7 0	7 0	9 6	70	97	53	30	31	32	

P07714 homo sapien	P05047 sarcophaga	P23806 trimeresuru	P43025 mus musculu	Q95198 macaca mula	028768 papio hamad	P23132 bos taurus	P43137 mus musculu	P83300 anser anser	095235 pondo pyqma	P98107 bos taurus	P26258 carcharhinu
PSPA_HUMAN	LECA_SARPE	IXA_TRIFL	TETN_MOUSE	LEM1_MACMU	LEM1_PAPHA	LITH_BOVIN	LIT1_MOUSE	ACAL_ANSAN	LEM1_PONPY	LEM2_BOVIN	TETN_CARSP
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248	283	152	202	372	372	175	165	132	372	485	166
12.5	12.5	12.4	12.4	12.3	12.3	12.2	12.1	12.1	12.1	12.1	12.0
	_	s.	8.5	7.5	37.5	136	135	34.5	34.5	34.5	134
139	139	138	13	13	H			٦	_	~	

#### ALIGNMENTS

		CC -: SIMILARITY: CONTAINS I C-TYPE LECTIN FAMILY DOMAIN.	<u> </u>	Nature 409:6	RA Hayashizaki Y.; RT "Functional annotation of a full-length mount obwa collection ".		Suzuki H., Toyo-oka	RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y. Storch K. F.	A. Nordone P. Ring B. Ringwald W. Rohataner I Cakamoto N.	KA GUSTINGION S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., RB IVONE D Marchional T Machine T Machine T	RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	A. A. A. M. I. M. Stanhli F. Surviki D. Pendia M. Markolo C., Quackenbush J., RA Schrim J. M. Stanhli F. Surviki D. Pomita M. Markor I. Mashid H.	RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	RA Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Salto R.	KA ATAKAWA T., HATA A., FUKUNISNI T., KOMOO H., AAACHI J., FUKUNA S., RA AISAWA K TISUS M Nichi W Kingama H MAAAA K.	RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	RX MEDLINE=21085660; Pubmed=11217851;			N. (2) author (CC1-2000) to the EmbLycenbank/UDBO databases.	RT chondrogenesis."; PT. Submitted (OCT-2000) to the EMBI (Compact Aptibuse)	"Mt75, a low expressed c-type lectin gene involving in				NCBI_TaxID=10090;		Eukaryota; Metazoa; Chordata;		DE CHODE. (Transmembrane protein MT/5).		DI 15-JUN-2002 (Rel. 41, Last sequence update)	15-JUN-2002	Q9CXM0; Q8VI31;	CHOD MOUSE STANDARD: DRT. 273 AA	RESULT 1
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Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asawa S.,
Shintani A., Sasaki T., Naqamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVPSREAEGEETELT 177
                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                                                                                                                          4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63
                                                                                                                                                                                                                                                                                                                                                                           Weng L., Smits P., Wauters J., Merregaert J.;
Molecular cloning and characterization of human chondrolectin, a
novel type I transmembrane protein homologous to C-type lectins.";
Genomics 80:62-70(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                           . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chondrolectin precursor (Transmembrane protein MT75) (PREDI2
                                                                                                                                                                                                                                                                                             51.5%; Score 574; DB 1; Length 273; 57.4%; Pred. No. 4e-44; Live 26; Mismatches 41; Indels
                                                                                                                                                                          POTENTIAL.
CTTOPLASMIC (POTENTIAL).
C-TYPE LECTIN.
N-LINEED (GLCNAC. . ) (PC
V -> W (IN REF. 2).
T -> K (IN REF. 2).
                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                     E052D933F244F4C7 CRC64;
         MGD; MGI:1920461; 310074E07R1K.
InterPro; IPR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615; CTYPE_LECTIN_1; FALSE_NEG.
Lectin; Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                 CHONDROLECTIN.
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SEQUENCE FROM N.A.
MEDLINE-20289799; PubMed-10830953;
                                                                                                                                                                                                                                                                     30303 MW;
BAB29226.1;
                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.4 Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 TPVLPEETQE 187
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CONFLICT
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21564202; PubMed-11707072; Reymond A.; Friedll M., Neergard Henrichsen C., Chapot F., Deutsch S., UCla C., Rossier C., Lyle R., Gulpponi M., Antonarakis S.E.; "From PREDs and open reading frames to cDNA isolation: revisiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOGUENCE OF 27-273 FROM N.A.
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Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Chiba T., Ishida S., Morakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                 Dagand E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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F4890AAFB572A311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 273;
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bl Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Da Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F. Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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60.1%; Pred. No. 5.2e-43;
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Genew: HGNC:17807; CHODL.
InterPro: IPPRO015; CLectin_C.
SWART; SM00034; CLECT; 1.
PROSITE: PSO00615; CTYPE_LECTIN_1; FALSE_NEG.
Lectin; Transmembrane: Glycoprotein; Signal.
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EMBL; AK022689; BAB14181.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF257472; AAL05981.1; -.
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL163217;
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4 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEK 63

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                            64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                                                                                                                                                                                                                                                                [3]
STUDIES ON THE BINDING OF INDIVIDUAL LECTIN DOMAINS.
MEDLINE-92112893; Pubmed=1730714;
Taylor M.E., Bezouska K., Drickamer K.;
"Contribution to ligand binding by multiple carbohydrate-recognition domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726(1992).
23 RVVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESEGGVLLSLENEAEQKLIES 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 642-788.
MEDLINE-20347275; PubMed-10779515;
Feinberg H., Park-Snyder S., Kolatkar A.R., Heise C.T., Taylor M.E.,
                                                                                                                                                                                                                                                                       Taylor M.E., Conary J.T., Lennartz M.R., Stahl P.D., Drickamer K.; "Primary structure of the mannose receptor contains multiple motifs resembling carbohydrate-recognition domains."; J. Biol. Chem. 265:12156-12162(1990).
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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"Organization of the gene encoding the human macrophage mannose
resentor (MRC1) ".
                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Macrophage mannose receptor precursor (MMR) (CD206 antigen).
                                                        119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVP 165
                                                                  PRT; 1456 AA
                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                              MEDLINE-90324192; PubMed-2373685;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-93052405; Pubmed-1294118;
                                                                                                                                                                                                                                                                                                                                                                       Genomics 14:721-727(1992).
                                                                                                                          STANDARD;
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PROSITE; PSO0615, C_TYPE_LECTIN_1; 6.
PROSITE; PSO0615, C_TYPE_LECTIN_2; 8.
PROSITE; PSO0123; FIBRONECTIN_2: 8.
PROSITE; PSO023; FICIN_BLECTIN, 1.
Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
SIGNAL 1 18
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FORM).
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FIBRONECTIN TYPE-II.
C-TYPE LECTIN 1 (LONG
C-TYPE LECTIN 2 (LONG
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
Fam; PF00040; fn2; 1.
Ffam; PF00659; lectin_C; 8.
Pfam; PF00659; Ricin_Blectin; 2.
PRINTS; PR00013; FNTYPEII.
ProDom; PD000995; FN_TYPEII; 1.
SWART; SM00059; FN_TYPEII; 1.
SWART; SM00059; FN_TYPEII; 1.
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PDB; 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
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M93203;
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MIM; 153618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINE-BALBC; TISSUE-Brain;
MEDLINE-96039250; PubMed-7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
Faessler R.,
"Structure and chromosomal localization of the mouse neurocan gene.";
Genomics 28:405-410(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 RREEKOSNSTACODLYAWIDGSISQFRNWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 MFQWNDDRCNMKNNFICKYSDEK----PAVPSREAEGEETELTTPVLPEETQE----- 187
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-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              21 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLR 80
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
104 N-LINKED (GLCNAC. . .) (POTENTIAL).
344 N-LINKED (GLCNAC. . .) (POTENTIAL).
529 N-LINKED (GLCNAC. . .) (POTENTIAL).
930 N-LINKED (GLCNAC. . .) (POTENTIAL).
1160 N-LINKED (GLCNAC. . .) (POTENTIAL).
1205 N-LINKED (GLCNAC. . .) (POTENTIAL).
1311 N-LINKED (GLCNAC. . .) (POTENTIAL).
1311 N-LINKED (GLCNAC. . .) (POTENTIAL).
AA; 166011 MW; 264E5AF3C576A5E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                                                                                                                                                               Length 1456;
                                                                                                                                                                                                                                                                                                                                                                                       61; Indels
                                                                                                                                                                                                                                                                                                                     Score 182; DB 1;
Pred. No. 2.8e-08;
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Last annotation update)
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(Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                   52; Conservative
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01-0CT-1996
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P55066;
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TD PGSON_MOUSE

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DE Neurocc

CO Mammal

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OC OC Selvary

OC Sel
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EGF-LIKE 1. EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal. SIGNAL 1 22 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE V-TYPE DOMAIN.
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N-LINKED (GLCNAC...
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31.5%; Pred. No. 6.6e-08;
tive 17; Mismatches 49
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BY SIMILARITY.
BY SIMILARITY.
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PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00122; BGF_2; 3.
PROSITE; PS01186; BGF_2; 1.
PROSITE; PS01187; BGF_CA; 1.
PROSITE; PS01615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
                                                             Interpro; IPRUCC...
Interpro; IPR01881; EGL_L...
Interpro; IPR003599; Ig.
Interpro; IPR003006; Ig_MHC...
A Interpro; IPR001304; Lectin_C...
---erpro; IPR000538; Link.
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LINK 2.
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Pfam; PF00008; EGF; 2.
Pfam; PF00047; 19; 1.
Pfam; PF00059; lectin_C; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                        SMART; SM00179; EGF_CA; 1.
SMART; SM0001; EGF_L1ke; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
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CLECT; 1.
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274
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SMART; SM00034;
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CARBOHYD
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TISSUE-Spinal cord;

MEDLINE-92062692; PubMed-1720020;

MEDLINE-92062692; PubMed-1720020;

Perides G., Bivlano F., Bignami A.;

Perides G., Bivlano F., Bignami A.;

Thereaction of a brain extracellular matrix protein with hyaluronic acid.";

Elochim. Biophys. Acta 1075:248-258(1991).

Connecting cells with the extracellular signaling and in connecting cells with the extracellular matrix. May take part in the requilation of cell motility, growth and differentiation. Binds hyaluronic acid.

C. ISUBCELLULAR LOCATION: Secreted; extracellular matrix.

ALTERNITY ENDUCTS: At least 4 isoforms; VO (shown here), VI, V2 and V3; are produced by alternative splicing.

C. ITISSUE SPECIFICITY: Cerebral white matter. VO and V1 are expressed in the central nervous system, and in a number of mesenchymal and epithelial tissues; the major isoform v2 is restricted to the central nervous system.

C. IDEVELORENTY STAGE: Disappears after the cartilage development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H., Zimmermann D.R.; Wersican V2 is a major extracellular matrix component of the mature bovine brain.";
                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                            PGCV_BOVIN STANDARD; PRT; 3381 AA.
P81282; 077609; 077610; 077612;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Chondroitin sulfate proteinprecursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3)
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MEDLINE-98288320; PubMed-9624174;
                       134 IGGPYMFQWNDDRCNMKNNFICK 156
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EMBL; AF060457; AAC24359.1; --
EMBL; AF060459; AAC24360.1; --
EMBL; AF060459; AAC24361.1; --
HSSP; P01132; 1EPG.
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InterPro; IPR000152; Asx\_hydroxyl.

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GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
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IG-LIKE V-TYPE DOMAIN.
LINK 1.
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C-TYPE LECTIN.
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Sushi_SCR_CCP.
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Interpro; IPR003600; Ig_like.
Interpro; IPR001304; Lectin_C.
Interpro; IPR000538; Link.
                                                                                                                                                                                                                                                                   Fram; PF00008; EGF; 2. Pfam; PF000047; 19; 1. Pfam; PF000047; 19; 1. Pfam; PF000049; sushi; 1. Pfam; PF00109; X11nk; 2. PRINTS; PR01265; LINKMODULE. PF00000; PD000918; Link, 1.
                            EGF_2.
EGF_Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-Spraque-Dawley; TISSDE-Brain;
MEDLINE-94406907; Pubmed=132657;
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
"Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroltin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19586-19547(1992).
                             POTENTIAL)
(POTENTIAL)
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16-0cT-2001 (Rel. 40, Last annotation update)
Neurocan core protein precursor (245 kDa early postnatal core glycoprotein) (Contains: 150 kDa adult core glycoprotein).
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25.5%;
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CSPG3 OR NCAN
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POSTNATAL AND ADULT BRAIN; NOT EXPRESSED
                                                                             -1 TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT BRAIN; NOT EXPRESSEE IN KIDNEY, LUNG, LIVER AND MUSCLE.
-1 PARI: COWTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-1 PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DECRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
-1 SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-1 SIMILARITY: CONTAINS 2 LINK DOMAINS.
-1 SIMILARITY: CONTAINS 1 LOTYPE LECTIN FAMILY DOMAIN.
-1 SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-1 SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteoglycan; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROCAN CORE PROTEIN.
150 KDA ADULT CORE GLYCOPROTEIN
IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Lectin; Sushi; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00022; EGF_1; 3.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01041; LINK; 2.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

Glycoprotein; Hyaluronic acid; Proteoqlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; P000918; Link; 2.
SNART; SN00032; CCP; 1.
SNART; SN00034; CLECT; 1.
SNART; SN00179; EGF CA; 1.
SNART; SN00109; EGF CA; 1.
SNART; SN00409; IG; 1.
SNART; SN004409; IG; 1.
PROSITE; PS00012; EGF_1; 3.
PROSITE; PS00012; EGF_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINK 1.
LINK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Link.
Sushi_SCR_CCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig.
Ig_MHC.
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000538; Li
InterPro; IPR000436; Su
Pfam; PF00008; EGF; 2.
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InterPro; IPR003006;
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J73 BY SIMILARITY.

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1040 BY SIMILARITY.

1149 BY SIMILARITY.

1156 1199 BY SIMILARITY.

1185 1121

BY SIMILARITY.

1187 121

N-LINKED (GLCNAC...) (POTENTIAL).

7 37 N-LINKED (GLCNAC...) (POTENTIAL).

7 37 N-LINKED (GLCNAC...) (POTENTIAL).

7 N-LINKED (GLCNAC...) (P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. N.A. (ISOFORM VINT).
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09ERB4, 008592, 088564, 09RIK4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Chondroitin sulfate proteins (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (FG-M) (Glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99327053; Pubmed-10397680;
Lemire J.M., Braun K.R., Maurel P., Kaplan B.D., Schwartz S.M.,
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MEDLINE-98308094; PubMed-9642104;
MILEV P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi
Margolis R.K., Margolis R.U.;
"Differential regulation of expression of hyaluronan-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blochem. Biophys. Res. Commun. 247:207-212(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 349-2738 FROM N.A. (ISOFORM VO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2421-2463 FROM N.A. (ISOFORM V0)
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MEDLINE-98094159; PubMed-9434070;
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958
975
1029
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967
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We c., Kristensen P., Ostergaard P.B., Othera! P.S., Romer J.:

RI, Wephron 77461-470(1997).

RI, Wephron 77461-400(1997).

RESPONDED OF 2535-2738 FROM M.A.

RESPONDED OF 2535-
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Chondroitin sulfate proteoglycan core protein 2) (PG-M)

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R -> RKWSFRKNGOPCFNKY (IN ISOFORM VINT).
AEREC -> NSARG (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 WIGLRRREEKQSNSTACQDLYAWIDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Caps
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(POTENTIAL)
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062059; Q62058; Q9CUU0;
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                           EGF-LIKE 1. CALCIUM-BINDING EGF-LIKE 2, CALCIUM-BINDING C-TYPE LECTIN. SUSHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; Indels
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2738 AA; 300004 MW; 12CA626D58BDBC6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
                                                                                                                                 BY SIMILARITY.
BY SIM
                                                            GAG-BETA
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Les 47; Conserv
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PGCV_MOUSE
ID PGCV_M
AC 062059
DT 01-NOV
DT 16-OCT
DE VERSIC
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Matches
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RA Acakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Radawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakawa T., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Fischmann W., Gassteriand T., Gissi C., King B., Kochiwa H., Rachim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bratincia M., Gariboldi M., Gariboldi M., Gariboldi M., Gariboldi M., Ramya M., Lee N.H., Rabaki M., Sato K., Stoch W., Mashima J., Mazarelli J., Momberts P., Asasaki H., Sato K., Stochabach C., Seya T., Shibata Y., Storch K.-F., Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Handal annotation of a fill control of a fil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: May play a role in intercellular signaling and in
connecting cells with the extracellular matrix. May take part in
the regulation of cell motility, growth and differentiation. Binds
hyaluronic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Secreted; extracellular matrix.
SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 4 isoforms; V0 (shown here), V1, V2 and V3; are produced by alternative splicing.
TISSUE SPECIFICITY: V2 is found only in brain.
DEWELOPMENTAL STAGE: Disappears after the cartilage development.
SIMILARITY: CONTAINS 1 IMMUNGLOBULIN-LIKE V-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: SONTAINS 1 SUSHI (SCR) DOMAIN.
                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1708I_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS VO; VI AND V2).
STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain;
MEDLINE=95122551; PubMed=7822335;
ILO K., Shinomura T., Zako M., Ujita M., Kimata K.;
"Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).
STRAIN-C57BL/6J; TISSUE-SKin;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues.";
J. Biol. Chem. 270:3914-3918(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6;
MEDLINE-95181355; PubMed-7876137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM V3).
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EMBL; D28599; -; NOT_ANNOT
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AND ISOFORM V3).

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17 ORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLONAC. ..) (POTENTIAL).
N-SING (IN ISOPORM V1).
MISSING (IN ISOPORM V2).
MISSING (IN ISOPORM V3).
A -> G (IN REF. 3).
I -> T (IN REF. 3).
I -> T (IN REF. 3).
TVWNSNS -> QFGIOTA (IN REF. 3).
                                                                                                                                                                                                                                                       15.6%; Score 174; DB 1; Length 3358; 28.5%; Pred. No. 3.8e-07; tive 23; Mismatches 55; Indels 4(
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mes 47; Conservative
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PGCV_HUMAN
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                                H MSDS; PULL124; LEGP.

H MCDS; MGI:102889; CSp92.

RICEPPO: IPR000152; Asx_hydroxyl.

RICEPPO: IPR000152; Asx_hydroxyl.

RICEPPO: IPR000152; Asx_hydroxyl.

RICEPPO: IPR000154; EGF_2.

RICEPPO: IPR001389; EGF_II.

RICEPPO: IPR001389; EGF_II.

RICEPPO: IPR001389; EGF_II.

RICEPPO: IPR001399; Ig.

RICEPPO: IPR001399; Ig.

RICEPPO: IPR001399; Ig.

RICEPPO: IPR000139; Sushi_SCR_CCP.

RICEPPO: IPR000139; Sushi_SCR_CCP.

RICEPPO: IPR000139; Link; I.

REMINIS; PR000109; EGFELOD.

REMINIS; PR000109; EGFELOD.

REMART; SM00019; EGFELOD.

REMART; SM00019; EGF_II.

REMART; SM0019; EGF_II.

REMART; SM0019; EGF_II.

REMART; SM0019; EGF_II.

REMART; SM00101; EGF_II.

REMART; SM0011; EGF_II.

REMART; SM0011; EGF_II.

REMART; EGF_II.

REMART; SM0011; EGF_II.

REMART; E
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
C-TYPE LECTIN.
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VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE DOMAIN.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
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MEDLINE-90059882;
Zimmernmann D.R., Ruoslahti E.;
Zimmernann D.R., Ruoslahti E.;
Whiltiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM V0).
MADLINE-95105188; PubMed-7520742;
Naso M.F., Zimmermann D.R., IOZZO R.V.;
"Characterization of the complete genomic structure of the human versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                                PGCV_HUMAN STANDARD; PRT; 3396 AA.
P13611; P20754; Q9UNM5; Q13010; Q13189; Q15123;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial CSPG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM V2).
TISSUE-Glial tumor;
MEDLINE-95105187; PubMed-7806529;
Dours-2inmermann M.T., Zinmermann D.R.;
"A novel glycosaminoglycan attachment domain identified in two alternative splice variants of human versican.";
J. Biol. Chem. 269:32998(1994).
                                                                                               132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
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an email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96213482; PubMed-8627343;
MEDLINE-96213482; PubMed-8627343;
Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
"Differential expression of versican isoforms in brain tumors.";
J. Neuropathol. Exp. Neurol. 55:528-533(1996).
-I- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95181355; PubMed-7876137;
Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
"Expression of PG-M(V3), an alternatively spliced form of PG-M
without a chondroitin sulfate attachment in region in mouse and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyaluronic acid.
SUBCELLUIAR LOCATION: Secreted; extracellular matrix.
SUBCELLUIAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 5 isoforms; V0 (shown here), V1, V3 and Vint: are produced and alternative splicing.
TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed in normal brain, gliomas, medulloblastomas, schwannomas, and menningiomas; V2 is restricted to normal brain medulloblastomas as is found in all these tissues except
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-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-I- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                Krusius T., Gehlsen K.R., Ruoslahti E.;
*A fibroblast chondroitin sulfate proteglycan core protein contains
Lectin-like and growth factor-like sequences.";
J. Biol. Chem. 262:13120-13125(1987).
                                                                                                                                                                                                                             IOzzo R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
McPherson J.D.;
Mapping of the version proteoglycan gene (CSPG2) to the long arm with the chromosome 5 (5q12-5q14).";
Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Versican/PG-M isoforms in vascular smooth muscle cells.";
Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porides G., Lane W.S., Andrews D., Dahl D., Bignami A.; "solation and partial characterization of a glial hydluronate-bloiding protein."
J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 270:3914-3918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Aortic smooth muscle;
MEDLINE-99327053; PubMed-10397680;
                                                                                                                                                                                  SEQUENCE OF 251-347 FROM N.A. MEDLINE-93122792; PubMed-1478664;
                                        TISSUE-Lung fibroblast;
MEDLINE-88007514; PubMed-2820964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
MEDLINE-89174663; Pubmed-2466833;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM V3).
[4]
SEQUENCE OF 2711-3396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                  rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wight T.N.;
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EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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SMART; SM00034; CLECT; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00019; EGF_CA; 1.

SMART; SM00010; EGF_Like; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

RARRT; SM00409; IG; 1.

RARTT; SM00409; IG; 1.

RARRT; SM00409; IG; 1.

RARRT; SM00409; IG; 1.

RARTT; SM00
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InterPro: IPR000542; EGF_11ke.
InterPro: IPR000542; EGF_2.
InterPro: IPR001481; EGF_C.
InterPro: IPR001481; EGF_C.
InterPro: IPR001481; EGF_II.
InterPro: IPR001306; Ig.
InterPro: IPR001306; Ig.
InterPro: IPR001306; Ig.
InterPro: IPR001306; Ig.MHC.
InterPro: IPR001304; Link.
InterPro: IPR001304; Link.
InterPro: IPR001436; Sushi_SCR_CCP.
Pfam; PP00059; Iectin_c; I.
Pfam; PP00059; Iectin_c; I.
Pfam; PP00059; Iectin_c; I.
Pfam; PP000193; X11nk; 2.
PKINTS; PR00010; EGFBLOOD.
Probom; PD0001018; Ilnk; 2.
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LINK 2.
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EMBL; U16306; AAA65018.1; -.
EMBL; X15998; CAA34128.1; -.
EMBL; S52488; AAB24878.1; -.
EMBL; U26555; AAA67565.1; -.
EMBL; D32039; BAA06801.1; -.
EMBL; J02814; AAA36437.1; -.
                                                                                                                                                                                AF084545; AAD48545.1;
                                                                                                                                                                                                            PIR; S06014; S06014.
PIR; A29348; A29348.
PIR; A30358; A30358.
HSSP; P01132; IEGF.
Genew; HGNC:2464; CSPG2.
MIM; 118661;
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                                                                                                                                                                                                                                   76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDF- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS: At least 2 isoforms; V0 (shown here) and V1; are produced by alternative splicing.
TISSUE SPECIFICITY: Prechondrogenic condensation area of
                                                 (POTENTIAL)
                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                    40;
                                                                                                                                                    (POTENTIAL)
                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                    Length 3396;
                                                                                                                                                                                  55; Indels
                                                                                                                                                                                                                                                                                    3275 -----QWNDVPCNYHLTYTCKKGTVACGOPPVVENAKTFGK 3310
                                                                                                                                                                                                                                                                    132 AGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGE 172
              BY SIMILARTY.
N.LINKED GLCNAC.
                                                                                                                                                                 ch 15.6%; Score 174; DB 1; Similarity 28.5%; Pred. No. 3.9e-07; 47; Conservative 23; Mismatches 55
                                                                                                                                 (GLCNAC.
(GLCNAC.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                             PRT; 3562 AA
                                                                                                                                 N-LINKED
N-LINKED
N-LINKED
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090953; 090945;
001-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequils-JUN-2002 (Rel. 41, Last anno
                                        615
782
809
332
398
                                                                                 1442
1468
1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyaluronic acid.
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
SUSHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid, 1.26
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
-!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSICAN CORE PROTEIN.
IG-LIKE V-TYPE DOMAIN.
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InterPro; IPR003599; IG.
InterPro; IPR001304; Lectin_C.
InterPro; IPR0001304; Lectin_C.
InterPro; IPR0001304; Lint.
Pfam; PF00004; Ig; 1.
Pfam; PF00004; Ig; 1.
Pfam; PF00004; Ig; 1.
Pfam; PF00009; Lectin_C; 1.
Pfam; PF00009; Lectin_C; 1.
Pfam; PF00009; Lectin_C; 1.
Pfam; PF000193; Link; 2.
SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00019; EGF_1ike; 1.
SMART; SM00001; EGF_1ike; 1.
PROSITE; PS00010; ASX_HYDROXIL; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01181; EGF_CA; 1.
PROSITE; PS01181; EGF_CA; 1.
PROSITE; PS01181; LINK; 2.
PROSITE; PS01181; LINK; 2.
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InterPro; IPRO00561; EGF-like.
InterPro; IPRO0142; EGF-2.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO03599; Ig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 WIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEP----SCGSEVCVVMYHQPSAP 131
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CD92T61; 09J1Z6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
16-JUN-2003 (Rel. 41, Last annotation update)
17-JUN-2003 (Cell 41, Last annotation update)
18-JUN-2003 (Cell 51, Last annotation update)
19-JUN-2003 (Rel. 41, Last sequence update)
19-JUN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=PVG; TISSUE-Natural killer cells;
STRAIN=PVG; TISSUE-Natural killer cells;
MEDLINE-20345218; PubMed=11093152;
Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
"Characterization and molecular cloning of rat ClqRp, a receptor on cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-WISTAR: TISSUE-Lung;
MEDLINE-20507883; PubMed-10934210;
Dean Y.D., McGreal E.E., Akatsu H., Gasque P.;
"Molecular and cellular properties of the rat AA4 antigen, a C-type lectin-like receptor with structural homology to thrombomodulin.";
                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%; Score 171; DB 1; Length 3562; 28.5%; Pred. No. 7.6e-07; ive 23; Mismatches 55; Indels 4
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SING (IN ISOFORM V1).
9BC566E88C1602D2 CRC64;
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                            N-LINKED GLCNAC...)
N-LINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388078 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Conservative
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1. Biol. Chem. 275:34382-34392(2000).

1. FUNCTION: Receptor (or element of a larger receptor complex) for Clq, mannose-binding lectin (MBLL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion.

1. SUBCELLULAR LOCATION: Type I membrane protein.

2. ITSSUE SPECIFICITY: Widely expressed Highly expressed in lung and heart. Expressed at lower level in brain, thymus, liver, spleen, intestine, kidney, adrenal gland, muscle and testis. Expressed on endothelial cells, platelates, undifferentiated monocytes and circulating natural killer cells.

2. ITMLARITY: CONTAINS I C-TYPE LECTIN FAMILY DOMAIN.

2. SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                           EGF-LIKE 2.

SEGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; PR000152; ASX_hydroxyl.

BrinterPro; IPR000152; ASX_hydroxyl.

BrinterPro; IPR001051; EGF-11ke.

BrinterPro; IPR001081; EGF-11ke.

BrinterPro; IPR001081; EGF-13ke.

BrinterPro; IPR001081; EGF: 5.

BrinterPro; IPR001081; EGF: 6.

BrinterPro; EGF: 6
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N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> K (IN REF. 2).
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C-TYPE LECTIN.
EGF-LIKE 1.
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FEBS
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15-JUN-2002 (Rel. 41, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
protein) (CSPCP).
                                                                                                                             57 EQKLIEKFIENLL----PSD---GDFWIGLRRREEKQSNSTACQDLYAWT-DGSISQFRN 108
                                                                                                                                                            WY-VDEPSCGSEVCVVMY-----HQPSAPAGIGGPYMFQWNDDRC-----NMKNNF 153
                                                                                                                                                                                  -----KWHESPCGTPDAPGNSIEGF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteoglycan
                                              Gaps
                                                                                  3 GRLLSGQP-----VCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESED 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87270630; PubMed-3111460;
oldberg A., Antonsson P., Heinegaard D.;
"The partial amino acid sequence of bovine cartilage proteoglycan,
deduced from a cDNA clone, contains numerous Ser-Gly sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perin J.-P., Bonnet F., Jolles J., Jolles P.;
Sequence data concerning the protein core of the cartilage
proteoglycan monomers. Characterization of a sequence allowing the
synthesis of an oligomoucheotide probe.";
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Cartilage;
MEDLINE-93352525; PubMed-8349621;
Meloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggreeans of different species. Evidence for a novel module.";
                                              46;
                     14.8%; Score 165; DB 1; Length 643; 25.2%; Pred. No. 3.5e-07; 1ve 35; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89380219; PubMed-2528543;
Antonsson P., Heinegaard D., Oldberg A.;
The keratan sulfate-enriched region of bovine cartilage pronsists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
9AE4C933AD943DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
                                                                                                                                                                                                                                                                                     2364 AA.
                                                                                                                                                                                  127 WYKASKSSCISKRCVSLILDLSLKPHPSHLP
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                                                                                                                                                                                                       154 ICKYSDEKPAVPSREAEGEETELTTP 179
                                                                                                                                                                                                                             178 LCKFNFKGMCSPLALGGPGQLTYTTP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arranged in homologous repeats.";
Biochem. J. 243:255-259(1987).
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MEDLINE-85027710; PubMed-6489519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2114-2150 FROM N.A.
                                                                                                                                                                                                                                                                                PGCA_BOVIN STANDARD; P
P13608; Q28159; P79117;
O1-JAN-1990 (Rel. 13, Last sequ
01-NOV-1997 (Rel. 35, Last sequ
15-JUN-2002 (Rel. 41, Last anno
68781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 563-1056 FROM N.A.
                                Local Similarity 25.2 ies 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
 643 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9913;
SEQUENCE
                      Query Match
                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
DOMAINS TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO
DOWNIN: TWO FIRE PROTECCIYCAN, WHILE ANOTHER GLOBULAR RECION,
MAKES UP THE C-TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFRATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                   -i- FUNCTION: THIS PROTEGGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALDRONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY PLAY A REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
-I- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
                                                                                                                              Perin J.P., Bonnet F., Jolles P.; ^{\circ} *Structural relationship between link proteins and proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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InterPro; IPR00181; EGF_2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001804; Ig-MHC.
InterPro; IPR001304; Lactin_C.
InterPro; IPR001304; SGXXSG.
InterPro; IPR001314; SGXXSG.
InterPro; IPR001314; SGXXSG.
InterPro; IPR001314; SGXXSG.
InterPro; IPR001314; Ig-Pfam; PF00018; EGF; 1.
Pfam; PF00019; IIInk; 4.
Pfam; PF00193; XIInk; 4.
Pfam; PF00193; XIInk; 4.
Propom; PF000191; IINk; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L07053; -; NOT_ANNOTATED_CDS.
PIR; A27752; A27752.
PIR; A29164; A29164.
PIR; E29164; E29164.
PIR; E29164; E29164.
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SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 4.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P08709; 1BF9.
InterPro; IPR00015; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
                                                                                                MEDLINE-87005253; PubMed-3530809;
Lett. 176:37-42(1984).
                                                                                                                                                                                                                            206:73-77(1986).
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SMART; SM00034; CLECT; 1.
                                                               PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGCA_HUMAN STANDARD; PRT; 2415 AA.
P16112, 013650;
01-APR-1990 (Rel. 14, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
PSGPCPA (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                          AA APPROXIMATE TANDEM REPEATS OF
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KED (GLCNAC. .) (POTENTIAL).

KED (GLCNAC. .) (POTENTIAL).

KED (GLCNAC. .) (POTENTIAL).

G (IN ISOFORM 2).
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BY
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                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushl;
ESF-like domain; Calciuum; Alternative splicing; Repeat;
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6FF83763420C3D4C CRC64;
                                                                                                                                                             AGGRECAN CORE PROTEIN IG-LIKE V-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%; Pred. No. 6.1e-06; ive 29; Mismatches 59
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SUSHI.
BY SIMILARITY.
EGF_CA; 1.
IG_MHC; FALSE_NEG.
LINK; 4.
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667 66
2114 215
2364 AA;
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                   PS00290; I
PS01241; I
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PROSITE;
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CARBOHYD
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PCCA_HOMAN
ID PCCA_HOLZ,
AC P16112,
DT 01-APR:
DT 15-JUM.
DE AGGTECG
GN AGCT OI OS
HOMO OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3, MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS) AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATLIX BIO1. 14:323-328(1994).
-1- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
-1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baldwin C.T., Reginato A.M., Prockop D.J.;
"A new epidermal growth factor-like domain in the human core protein
for the large cartilage-specific proteoglycan. Evidence for
alternative splicing of the domain.";
J. Biol. Chem. 264:15747-15750(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAINS, N-LINKED AND O-LINKED OLIGOSACCHÁRIDES.
--- SIMILARITY: CONTAINS 1 IMMONGCIGABULIN-LIKE V-TYPE DOMAIN.
--- SIMILARITY: CONTAINS 4 LINK DOMAINS.
--- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: CONTAINS 1 SUGHI (SCR) DOMAIN.
--- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROFEOGLYCAN FAMILY.
                                                                                                                                                 Doege K.J., Sasaki M., fillura T., Yamada Y.; and J. Sasaki M., fillura T., Yamada Y.; and J. Sasaki M., fillura T., Yamada Y.; and large aggregating proteoglycan, aggregating proteoglycan, aggregating proteoglycan, aggregating proteoglycan, and additional alternatively spliced forms."; J. Blol. Chem. 266:894-902(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILATILY)
ALTERNATIVE PRODUCTS: THERE ARE AT LEAST 3 FORMS OF AGGRECAN
TRANSCRIPTS GENERATED BY ALTERNATIVE EXON USAGE. THE SHORTEST
ALSO THE MOST PREVALENT FORM, LACKS BOTH THE EGF-LIKE DOMAIN,
SUSHI DOMAIN.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barry F.P., Neame P.J., Sasse J., Pearson D.; "Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                               TISSUE-Chondrocytes;
Dudhia J., Hardingham T.E.;
Submitted (JAN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                          OF 1-2162; 2201-2329 AND 2391-2415 FROM N.A
                                                                                                                                                                                                                                                                                            SEQUENCE OF 1778-2162 AND 2201-2415 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1936-2415 FROM N.A. MEDLINE-89380154; Pubmed-2789216;
                                                                                                                 TISSUE-Chondrocytes;
MEDLINE-91093289; PubMed-1985970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95128522; PubMed-7827755;
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EMBL; J05062; AAA35726.1; -.
EMBL; X17406; CAA35463.1; -.
EMBL; S74659; AAC60643.2; -.
PIR; S08042; S08042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND G3
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                                                                                              SEQUENCE
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2002 QEVCEEGWINKYQGHCYR--HFPD---RETWYDAERRCREQQSHLSSIVTPEEQ----EFV 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGCA_CANFA STANDARD; PRT; 2333 AA.
028343; 028310;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-protein (CSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Glant T.T., Adams M.E., Kwok S.X.F., Huang D., Fulop C.; Complete coding sequence and deduced amino acid sequence of aggrecan of canine cartilage...; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 268:17377-17383(1993).
-1- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR MATRIX OF CARTILAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 VVM-YHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYS----DEKPAVPSREAEGEETE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 QPVCRGG----TQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFI 65
                                                                                                                                                                                                                                                                                     .) (POTENTIAL).
2 AND ISOFORM 3)
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2082-2118 FROM N.A.
TISSUE-Cartilage;
TISSUE-93352525; PubMed-8349621;
Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like domains in aggrecans of different species. Evidence for a novel
                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                    ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.2%; Score 158.5; DB 1; Length 2415; Best Local Similarity 29.1%; Pred. No. 6.3e-06; Matches 52; Conservative 22; Mismatches 62; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 774-833 FROM N.A.
TISSUE-Cartilage;
MEDLINE-951255 PubMed-7827755;
Barry F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                657 N-LINKED (GLCNAC. . .) (POTENT 1898 N-LINKED (GLCNAC. . .) (POTENT 2200 MISSING (IN ISOFORM 2 AND ISOFORM 2.) (POTENT 2390 MISSING (IN ISOFORM 3).  
766 E -> A (IN REF. 4).  
847 E -> A (IN REF. 4).  
1928 E -> A (IN REF. 2).  
1964 I -> V (IN REF. 2).  
1964 I -> V (IN REF. 2).  
2307 P -> A (IN REF. 2).  
2331 A -> P (IN REF. 2).  
2331 A -> P (IN REF. 2).  
2341 A -> P (IN REF. 2).  
2341 A -> P (IN REF. 2).  
2351 A -> P (IN REF. 3).  
2351 A -> P (IN REF. 3).  
250191 MW; 1288937E1B98C6B6 CRC64;
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Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggrecan.";
Matrix Biol. 14:323-328(1994).
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PGCA_CANFA
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                                                                                                                                                                                                   -I- FTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 1 LINK DOMAINS.
-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-I- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-I- SIMILARITY: CONTAINS 1 BGF-LIKE DOMAIN.
-I- SIMILARITY: CONTAINS 1 BGF-LIKE DOMAIN.
-I- SIMILARITY: CONTAINS 1 BGF-LIKE DOMAIN.
                                                                   SIMILATILY).
DOMAIN: TWO GLOBULAR DOMAINS, G1 AND G2, COMPRISE THE AMINO
TERMINUS OF THE PROTEOGLYCAN, WHILE ANOTHER GLOBULAR REGION, G3,
MAKES UP THE COOH TERMINUS. G1 CONTAINS LINK DOMAINS AND THUS
CONSISTS OF THREE DISULFIDE-BONDED LOOP STRUCTURES DESIGNATED AS
THE A, B, B' MOTIFS. G2 IS SIMILAR TO G1. THE KERATAN SULFATE (KS)
AND THE CHONDROITIN SULFATE (CS) ATTACHMENT DOMAINS LIE BETWEEN G2
                       PLAY
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LINK 4.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION. MAY REGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE. SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010, ASK, HYDROXYL; 1.
PROSITE; PS00012, EGF_1; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01241; LINK; 4.
PROSITE; PS01241; LINK; 4.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
Glycoprotein; Cartilage; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain; Repeat; Immunoglobulin domain.
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IG-LIKE V-TYPE DOMAIN.
LINK 1.
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InterPro; IPR000151; EGF-11ke.
InterPro; IPR000142; EGF-2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001809; Ig.
InterPro; IPR001806; Ig_MHC.
InterPro; IPR001818; Lectin_C.
InterPro; IPR001818; Link.
InterPro; IPR001818; SGXXSG.
InterPro; IPR0001818; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U65989; AAB06238.2; -.
EMBL; S74662; AAC60527.1; -.
EMBL; L07054; -: NOT_ANOTATED_CDS.
HSSP; P08709; 1BF9.
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SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Selectin precursor (Endothelial leukocyte adhesion molecule 1)
(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)
(CD62E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                     C. . ) (POTENTIAL).
                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                               Length 2333;
                                                                                                                                                                                                                                                                                                              8B9ED78F3508B596 CRC64;
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llarity 28.5%; Pred. No. 1.1e-05;
Conservative 24; Mismatches 61;
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MEDLINE-92283265; PubMed-1375914;
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                                                                                                           MEDINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-1378846;

MEDLINE-92340571; PubMed-13788618;

MEDLINE-24; MEDLINE STATE STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
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InterPro: IPR001361; EGF-like.
InterPro: IPR001361; Lectin_C.
InterPro: IPR001365; Selectin_C.
InterPro: IPR001365; Selectin_C.
InterPro: IPR000436; Sushi_SCR_CCP.
Pfan; PF00084; Sushi_C: 1.
Pfan; PF00084; Sushi; 6.
PRINTS; PR00143; SELECTIN.
SMART; SM0014; CLECT; 1.
SMART; SM00181; EGF; 1.
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EMBL; M87862; AAA37577.1; ALT_INIT.
HSSP; P16581; 1KJA.
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BY SIMILARITY. BY SIM	tch al Similarity 27.9%; Score 154.5; DB 1; Length 612; 38; Conservative 28; Mismatches 45; Indels 25; Gaps YFHDTSRRLNFEEAKEACREDGQLVSIESEDEQKLIEKFIENLLPSDCDFWIGLRRREE 84  :::
3300 3350 3350 4413 4413 4426 4489 523 523 331 528 666 6749 M	13.9%; 27.9%; 27.9%; vative  AKEACREDG               ssarcordy  #TDGSI         wycgckPLT  #YGGKPLT  #YGGKPLT  ALC 138
273 3368 3368 3368 4431 4431 192 1145 1145 1145 1145 1145 1145 1145 114	al Similarity 27.  38; Conservative YFHDTSRRLNFEEAKEACR  :::  ::    : YNASSELMTYDEASAYCO) KQSNSTACQDLYAWTDGSVNNWHWWGTGK  ::
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Search completed: May 20, 2003, 17:05:30 Job time : 19 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 20, 2003, 17:02:46; Search time 31 Seconds (without alignments) 1369.216 Million cell updates/sec Run on:

Title: Perfect score:

US-09-887-855-5 1115 1 ATGRLLSGOPVCRGGTORPC......EEDAKKTFKESREAALNLAY 206 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_21:\*
1: Sp\_archea:\*
2: Sp\_bacteria:\*
3: Sp\_fungi:\*
5: Sp\_human:\*
5: Sp\_human:\*
5: Sp\_nhc:\*
5: Sp\_ncdent:\*
5: Sp\_ntrus:\*
5: Sp\_unclassified:\*
5: Sp\_unclassified:\* sp\_rvirus:\* sp\_bacteriap:\* sp\_archeap:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Description	O96nf3 homo sanien	OBTAVA homo ganton	096nc5 homo sapien	092209 Omor. 002200	ORVINI mus musoul:	Object of the cutton	Of 1830 min minorial	025100 bridge atten	One of the second	USYSPS nomo sapten	Q9ubg0 homo sapien	Q9upk6 homo sapien	O14594 homo santen	064449 mms missing	Obviva budra meani	THE THE TAKE OF THE THE	Mayire mus musculu	062623 bos taurus
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		9400	3007	1115	1115	1111	945.5	574	185	178.5	177.5	176.5	176.5	1	9/1	176	170.5	161.5	159.5		108.0
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Q912W4 Q9D8V4 Q912X0 Q90W17 Q95244	Q90WAZ Q90WI6 Q28008 Q22136	Q27340 Q9NT67 Q9HBK4 Q96GW7 Q96FP7	Q8TBB9 Q20665 Q8SQB2 Q9EPW4 Q95LC6 Q95J96	Q9DG39 Q25459 Q8WSX2 P79787 Q9UB05 Q95LA8
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158 158 158 157	152.5 152.5 152 149.5 149.5		148.5 148 148 147 147	146.5 146.5 146.5 145.5 145.5
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## ALIGNMENTS

50.0	Q96NF3 PRELIMINARY; PRT; 374 AA. Q96NF3;	01-DEC-2001 01-DEC-2001		CDNA FLJ309			buvalyola; Metazoa; Unordata; Uraniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.	NCBI_TaxID=9606;		SEQUENCE FROM N.A.		Watanabe M., Fulimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.	Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,	Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,	Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,	Magatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,	"NEDO human cDNA sequencing project.":	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	EMBL; AK055539; BAB70946.1;	InterPro; IPR001304; Lectin_C.	Program Pr00059; lectin_c;	PROSITE; PSSUU41; C_TYPE_LECTIN_2; 1. SEQUENCE 374 AA; 42280 MW; 8AE64E6BC9E56DCD CRC64;	Ouery Match 100.0%: Score 1115: DR 4: Length 374:	Similarity 100.0%; Pred No. 3.86-98;	6; Conservative 0;	1 ATGRILISGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 60	22 ATGRILISGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL 81
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ31092 fis, clone IMR321000158, highly similar to Cricetulus
1 ATGRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawal-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC025407; AAH22407.1; -.
SEQUENCE 374 AA; 42312 MW: FC214E6BC9E578D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to unnamed protein product.
                                                                                                                                                                                                                                                                                                                          374 AA
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ID 08TAY8

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Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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Borowsky M.L., Hynes R.O.;

Borowsky M.L., Hynes R.O.;

"Layilin, a novel talin-binding transmembrane protein homologous with
"Layilin, a novel talin-binding transmembrane protein homologous with
C-type lectins, is localized in membrane ruffles.";
J. Cell Biol. 143:0-0(1998).

EMBL; AF093673; AAC68695.1; -.

HSSP; P06734; 1HLI.

Interpret Interpret Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                   22 ATGRILISGOPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGRILSGOPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIE
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                                                                                                                                                                                                                                                 Length 374;
                                                  Indels
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SPOURINCE 374 AA; 42435 MW; 298ABBA24FB04E1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 5.5e-82;
                                                                                                                                                                                                                                               Score 1111; DB 4;
Pred. No. 9.2e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%; Scor.
85.9%; Pred. No. 5...
                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.68;
                                                                                                                                                                                                                                                                al Similarity 99.5
205; Conservative
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Best Local S:
Matches 205,
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77 IGLRRREEKQSNSTACODLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMY-HQPSAPA 132
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
   "Coordinate Regulation of Cadherin and Integrin Function by the Chondroitin Sulfate Protecolycan Neurocan.";
J. Cell Biol. 149:1275-1228(2000).
EMBL; AFI16856; AAD24546.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PRINTS; PROMO315; ALINK; 2. |
| PRINTS; PROMO315; ALINK; 2. |
| PRINTS; PROMO312; CCP; 1. |
| SMART; SMO0032; CCP; 1. |
| SMART; SMO0032; CCP; 1. |
| R SMART; SMO0103; EGF_CA; 1. |
| R SMART; SMO0103; EGF_Like; 1. |
| SMART; SMO0104; EGF_Like; 1. |
| SMART; SMO0104; EGF_Like; 1. |
| PROSITE; PSO0010; ASZ_HYDROXYL; UNKNOMN_1. |
| PROSITE; PSO0012; EGF_LECTIN_1; 1. |
| PROSITE; PSO1186; EGF_2; 1. |
| PROSITE; PSO1186; EGF_2; 1. |
| PROSITE; PSO1187; EGF_CA; 1. |
| PROSITE; PSO1131; LINK; 2. |
| PROSITE; PSO1131; LINK; 2. |
| PROSITE; PSO1134; LINK; 2. 
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Last annotation update)
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MEDLINE-93043353; Pubmed-1421407;
Harris N., Rits M., Chang G., Ezekowitz R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                            Interpro: IPR000152; Asx_hydroxyl.
Interpro: IPR000561; EGF-11ke.
Interpro: IPR000742; EGF_2.
Interpro: IPR001481; EGF_Ca.
Interpro: IPR001438; EGF_II.
Interpro: IPR003006; Ig_MHC.
Interpro: IPR003006; Ig_MHC.
Interpro: IPR0033006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
Pfam; PF00047; 19; 1.
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nes 50; Conserv
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Neurocan core protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 FIENLLP----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPSCGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 EVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE-KPAVPSREAEGEETELT 177
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                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
C-type lectin protein MT75.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.5%; Score 574; DB 11; Length 273; Best Local Similarity 57.4%; Pred. No. 9.9e-47; Matches 109; Conservative 26; Mismatches 41; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weng L., Smits P., Hubner R., Wouters J., Merregaert J.;
"Mt75, a low expressed c-type lectin gene involving in chondrogenesis."
Submitted (CT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF311699, AAL50354.1;
InterPro; IPR001304; Lectin_C.
FROSTE: PRO0059; lectin_c: 1.
SMART: SM00034; CLECT; 1.
FROSITE: PS50041; C_TYPE_LECTIN_2; 1.
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SEQUENCE FROM N.A.
MEDLINE-20309833; PubMed-10851024;
Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
                                                                                                                                                                                                                                                                                               273 AA.
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                                                                                        182 PEETQEEDAKKTFKESREAALNLAY 206
                                                                                                                       204 PEETQKEDTKETFKESREAALNLAY 228
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STRAIN-IRLING.
MEDILINE-20209407; PubMed-10744720;
MEDILINE-20209407; PubMed-10744720;
MEDILINE-20209407; PubMed-10744720;
"Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type Lectin-like Extracellular Domains.";
J. BAOL. Chem. 275:10323-10330(2000).
EMBL; L25612; AAA29218-2; ---
HSSP; P11362; IFGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 178.5; DB 11; Length 1456; 25.9%; Pred. No. 3.7e-08; Ative 33; Mismatches 66; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine Kinase receptor.

Hydra attenuata (Hydra) (Hydra vulgaris).

Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;

Hydridae; Hydra.

NCBI_TaxID=6087;
"Characterization of the murine macrophage mannose receptor.";
Blood 80:2363-2373(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR SEQUENCE 1456 AA; 165065 MW; 4EBD3F1BB619A594 CRC64;
                                                                                                                                                            Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases EMBL; 211974; CAA78028.1; -. HSSP; P22897; 1EGG.
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01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                     MGD: MGI:97142; MGD:
InterPro; IPR000562; FN_Type_II.
InterPro; IPR000562; FN_Type_II.
InterPro; IPR00070364; Lectin_C.
InterPro; IPR00070364; Lectin_C.
Pfam; PF00040; fn2; 1.
Pfam; PF00052; Ricin_B_lectin, 2.
PRINTS; PR00013; FNTYPE_II; 1.
SMART; SM00014; CLECT; 8.
SMART; SM00059; FN_TYPE_LECTIN_I; 6.
PROSITE; PS00015; C_TYPE_LECTIN_I; 6.
PROSITE; PS00012; FIBRONECTIN_I; 6.
PROSITE; PS00013; FIBRONECTIN_I; 1.
PROSITE; PS00013; FIBRONECTIN_I, 1.
PROSITE; PS00013; FIBRONECTIN_I; 1.
PROSITE; PS00013; FIBRONECTIN_I; 1.
PROSITE; PS00013; FIBRONECTIN_I; 1.
PROSITE; PS00013; FIBRONECTIN_I; 1.
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1456
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SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
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SEQUENCE
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                                                                                                                                             MEDLINE-98403880; PubMed-9734811;
Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Nomura N., Ohara O.;
Trediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
EMBL; AF107292; AAF14192.1; -.
EMBL; AF107292; AAF14192.1; -.
EMBL; AF107292; AAF14192.1; -.
                                                                                          67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                            7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                          DB 4; Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.8%; Score 176.5; DB 4; Length 1479; Best Local Similarity 30.4%; Pred. No. 5.8e-08; Matches 51; Conservative 25; Mismatches 57; Indels 35;
                       Query Match 15.8%; Score 176.5; DB 4; Length 1
Best Local Similarity 30.4%; Pred. No. 5.8e-08;
Matches 51; Conservative 25; Mismatches 57; Indels
                                                                                                                                                                                              124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
166669 MW; 9F4BAF355F036FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding properties.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;
                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Urokinase receptor-associated protein UPARAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000562; FN_Type_II.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000766; Lipocln_CytFABP.
InterPro; IPR00072; Ricin_B_lectin.
Pfam; PF00069; Iectin_C; 8.
PRINTS; PR00013; FNTYPEII; I.
SWART; SW00013; FNTYPEII; I.
SWART; SW000595; FN_Type_II; I.
SWART; SW00059; FN_I, I.
SWART; SW00659; FN_I, I.
PROSITE; PS00615; C_TYPE_LECTIN_I; 8.
PROSITE; PS00615; C_TYPE_LECTIN_I; 8.
PROSITE; PS00013; FIBRONECTIN_2; UNKNOWN_I.
PROSITE; PS00013; IIPROCALIN; UNKNOWN_I.
PROSITE; PS00213; RICIN_B_LECTIN, I.
PROSITE; PS00213; RICIN_B_LECTIN, I.
PROSITE; PS00213; RICIN_B_LECTIN, I.
PROSITE; PS00213; RICIN_B_LECTIN, I.
                                                                                                                                                                                                                                                                          PRELIMINARY;
1479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
SEQUENCE
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Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankhelm M., Amico-Reller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Krommiller B., Arellano A., Montgomerry M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of an -1 Mb region containing the MEF2B gene in
67 NLLPSDGDFWIGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                          SEVE---ELMIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFEPNNFRDSLEDCVT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00104; CLECT; 1.
SMART; SM00101; EGF_CA: 1.
SMART; SM00010; EGF_CA: 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS00015; CITPE_LECTIN_1; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_3.
PROSITE; PS01186; EGF_1; UNKNOWN_3.
PROSITE; PS01186; EGF_2: 1.
PROSITE; PS01186; EGF_2: 1.
Calcium-binding; EGF_1ike domain; Glycoprotein; Repeat.
                                                                                                                                                                                                                                               124 MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEG 171
                                                                                                                                                                                                                                                                                        Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005254; AAC25581.1; -.
HSSP; P00740; 1EDM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PGCN_HUMAN, partial CDS (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000761; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001081; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; Sushi_SCR_CCP.
Ffam; PF00008; EGF; 2.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00064; Sushi; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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32; Gaps

48; Indels

Mismatches

18;

Conservative

us-09-887-855-5.rspt

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45;
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Matches
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         Matches
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90 QGHCYR--YF---AHRRAWEDAEKDCRRRSGHLTSVHSPEEHSFINSF-----GHENTW 138
                                                          77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 133
                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-99013874; Pubmed-9795216;
Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G.;
"Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K., Christensen M., Gordon L., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L., Bruce R., Quan G., Montgomery M., Ow D., Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, ARC05657; AAC865561; --
EMBL, AC003110; AAB86655.1; --
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1321;
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PROSITE; PS01187; EGF_CA; 1.
PROSITE: PS01241; LINK; 2.
Calcium-binding; EGF-1ike domain; Glycoprotein; Repeat.
SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 5.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO019; EGE_CA; 1.
SMART; SMO0109; EGE_CA; 1.
SMART; SMO0409; EGE_11ke; 1.
SMART; SMO0445; LIKK; 2.
PROSITE; PSO0010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PSO00110; ASY_HYBE_LECTIN_1.
PROSITE; PSO0041; C_TYPE_LECTIN_1.
PROSITE; PSO0022; EGF_1; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003599; Ig.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001304; Lectin_C.
Interpro; IPR000538; Link.
Interpro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPRO00152; Asx_hydroxyl.
IPRO00561; EGF-like.
IPRO00742; EGF_2.
IPRO01881; EGF_Ca.
                                                                                                                                                                                       134 IGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                               188 -----RWNDVPCNYNLPYVCK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%;
31.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00008; BGF; 2.
Pfam; PF00047; 19; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushl; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-990 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000918; Link; 2. SMART; SMO032; CCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurocan (PGCN_HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
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SM00179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSPG3 OR NEUR
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10 - JAA

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Best Local Similarity

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RAY W. K., Yuan J., Lasky L.A.;

RY TUDE 103201; Tudecard of a novel member of the macrophage mannose receptor type C lectin family.

J. Biol. Chem. 271:21323-21330(1996).

REMED: U56734; AAC5729-1; ...

BRID: P02751; 2FN2.

BRID: MGD: MGC: IPR001028; FN Type_II.

RICEPTO: IPR0010565; FN Type_II.

RICEPTO: IPR000566; Lipoch_C, FN Type_II.

RICEPTO: IPR000566; Lipoch_C, FN Type_II.

RICEPTO: IPR000772; Ricin_B_lectin.

BRART: PF00040; FN2.

BRART: SP00040; FN2: 1.

REMED: PF00059; FN2: 1.

PROSITE; PS00045; FN2: 1.

BRART: SN00458; RNZYPE_LECTIN_1; 3.

PROSITE; PS00045; C_TYPE_LECTIN_1; 3.

PROSITE; PS00045; C_TYPE_LECTIN_2; B.

PROSITE; PS00045; C_TYPE_LECTIN_2; B.

PROSITE; PS00045; C_TYPE_LECTIN_1; 3.

PROSITE; PS00045; RICIN_B_LECTIN_1; 3.

PROSITE; PS00241; RICIN_B_LECTIN_1; 1.

PROSITE; PS00241; RICIN_B_LECTIN_1; 1.

PROSITE; PS00241; RICIN_B_LECTIN_1; 1.

PROSITE; PS00241; RICIN_B_LECTIN_1; 1.
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                                                                                                                                                   77 IGLRRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVVMYHQPSAPAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 NLLPSDGDFWIGLRREEKQSNSTACQDLYAWTDGSISQFRNWYVDEPS---CGSEVCVV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 QRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFW 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFIE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 170.5; DB 11; Length 1479; 31.4%; Pred. No. 2.2e-07; ive 22; Mismatches 48; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| || ::||
-----RWNDVPCNYNLPYVCK 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-96355501; Pubmed-8702911;
                                                                                                                                                                                                                         134 IGGPYMFQWNDDRCNMKNNFICK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20, Lectin lambda.
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                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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S W D D R D D R D D R S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 CY--FFQNKTLQAKNWRDASLSCQALGGHLLSIEDQAENFFILNFLKDSSMQQDNYWIGL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21575692; PubMed-11718900;
MEDLINE-21575692; PubMed-11718900;
Nakamura K., Funakoshi H., Tokunaga F., Nakamura T.;
"Molecular cloning of a mouse scavenger receptor with C-type lectin (SRCL)(1), a novel member of the scavenger receptor family.";
Blochim. Blophys. Acta 1522:53-58(2001).
EMBL; AB038519; BAB82497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20209407; PubMed-10744720;
Refaling J.C., Miller M.A., Steele R.E.;
"Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
Lectin-like Extracellular Domains.";
J. Biol. Chem. 275:10323-10330(2000).
EMBL; AF129528; AAD30040.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                             Eukaryotá; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
NCBI_TaxID=6085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 161.5; DB 5; Length 134; 28.8%; Pred. No. 8.9e-08; tive 23; Mismatches 51; Indels 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AA; 15701 MW; E7B7211C881009BC CRC64;
                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Receptor protein-tyrosine kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SCAVENGER receptor with C-type lectin.
COLECI2 OR SRCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Kinase: Tyrosine-protein kinase.
134 134 134
                                                                                                      134 AA
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                                                                                                                                                                                                                                                                                                        Hydra magnipapillata (Hydra)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||: |: | |||||
----WNDENCDATNGFICK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                   Q9XYX3
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OBVIF6;
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QBVIF6
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